

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2006, 22:50:52 ; Search time 254 Seconds
(without alignments)
8229.971 Million cell updates/sec

Title: US-10-626-126-6

Perfect score: 1176

Sequence: 1 atgtcggagtctaacggcac.....cccgatcagtatcttcttga 1176

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PE COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	669	56.9	1173	3	US-09-414-010-1
2	669	56.9	1173	3	US-09-812-216-1
3	669	56.9	1173	3	US-09-875-076-13
4	158.4	13.5	1239	3	US-09-891-053-2
5	158.4	13.5	2700	3	US-09-891-053-5
6	138.4	11.8	1335	2	US-08-985-090-3
7	138.4	11.8	1335	3	US-09-165-543-3
8	138.4	11.8	1335	3	US-09-167-354-6
9	138.4	11.8	1335	3	US-09-642-855-6
10	138.4	11.8	1335	3	US-09-642-514-6
11	138.4	11.8	1335	3	US-09-642-852-6
12	138.4	11.8	2050	3	US-09-891-053-21
13	138.4	11.8	2665	3	US-09-949-016-5059
14	138.4	11.8	2689	2	US-08-985-090-1
15	138.4	11.8	2689	3	US-09-165-543-1
16	138.4	11.8	2699	3	US-09-167-354-5
17	138.4	11.8	2699	3	US-09-642-855-5
18	138.4	11.8	2699	3	US-09-642-514-5
19	138.4	11.8	2699	3	US-09-642-852-5
20	138	11.7	1338	3	US-09-165-543-6
21	138	11.7	1953	3	US-09-891-053-26
22	138	11.7	3244	3	US-09-165-543-4
23	89	7.6	1056	3	US-09-524-162-1
24	88.8	7.6	1086	2	US-08-985-090-6

ALIGNMENTS

RESULT 1

US-09-414-010-1
; Sequence 1, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414,010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-414-010-1

Query Match	56.9%	Score 669;	DB 3;	Length 1173;
Best Local Similarity	74.2%	Pred. No. 6.3e-218;		
Matches	875;	Conservative	0;	Mismatches 295;
Indels	9;	Gaps	2;	
Qy	1	ATGTCGGAGTCTAACGGCACTGACGCTTGCCTGCTGCTCAAGTCCCTTGGCATTT	60	Sequence 33, Appl
Db	1	ATGCCAGATACTAATAGCAACAATTTATCATAGCACTCGTGTACTTTAGCATTT	60	Sequence 4, Appl
Qy	61	TTAATGTCCTGCTTGTCTTTGTATAACGATAGGCAATGCTGTGTCATTTAGCCCTTT	120	Sequence 31, Appl
Db	61	TTTATGTCCTTAGTAGCTTTGTCTAATATGCTAGGAATGCTTGTGTCATTTAGCTTT	120	Sequence 514, App
Qy	121	GTACGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT	180	Sequence 1, Appl
Db	121	GTGTGGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAATTTGGCCATCTCT	180	Sequence 177027,
Qy	181	GACTTCTTCTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACAGCTGTTAACTGG	240	Sequence 13, Appl
Db	181	GACTTCTTCTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACAGCTGTTAACTGG	240	Sequence 16801, A
Qy	241	AATTTTGGAGTGAATCTGCATGTTTTTGGCTCACTACTGACTATCTTTTGTGCACAGCA	300	Sequence 512, App
Db	241	GATTTTGGAAAGGAATCTGTGTAATTTTGGCTCACTACTGACTATCTTTTGTGCACAGCA	300	Sequence 8, Appl

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Db 301 TCTGTATATACATGTTGCTCTCATCAGCTATGATGATACCTGTCAGTCTCAATAGCTGTG 360
QY 361 CGTTATAGACACAGCACACTGGCATCCTGAAATTTGTTCTCAAAATGGTGGCTGTTGG 420
Db 361 TCTTATAGAACTCAACATACTGGGCTCTGAAGATTGTTACTCTGATGGTGGCGGTTGG 420
QY 421 ATACTGGCTTTCTTGGTCAATGCGCCNAATGATTTCTGGCTTCGGATTTCTTGGAAAGACAGC 480
Db 421 GTGCTGGCTTTCTTAGTGAATGGCCAAATGATTTCTAGTTTTCAGAGCTTTGGAAAGGA --- 476
QY 481 ACCAACACAGAGAGAGTGGAGCTGGCTTTGTTACTGAGTGGTACATCTCTCGCCATTACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTTGCATCAC 534
QY 541 GCATTTCTTGGAAATTCCTGCTCCCTGCTCTCCTTGGTGGTCTATTTTCAGTGTACAGATTTAC 600
Db 535 TCATTTCTTGGAAATTCGTGATCCAGTCATCTTAGTGGCTTATTTCAACATGAATATTTAT 594
QY 601 TGAAGCTGTGGAAGCTGGAGTCTCAGTAGTGCCCTAGCCACCGTGGATTCATCGCT 660
Db 595 TGAAGCTGTGGAAGCTGGATCATCTCAGTAGTGCCCAAGCCATCTCTGACTGACTGCT 654
QY 661 ACCTCTTCAGGGGCACTGACACTCAGCAGAACTGGGTGGTGGTGTAGGCAAGCTTT 720
Db 655 GTCTCTTCCAAACATCTGGACACTCAATCAGAGGTAGACTATCTCAAGGAGATCTCT 714
QY 721 CCTGGATTTAAGGAACAGCGCCGATCCCTTCATTACAGAAAGTCCACGAGGAAGAGCAGT 780
Db 715 TCTGCATCGACAGAGTTCTGATCCTTCATCTCAGAGAGACAGAGGAGAGAGTAGT 774
QY 781 CTCTGCTGTCTTAAGGACTCAATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
Db 775 CTCAATGTTTCTTCAAGAACCAAGATGAATAGCAATCAATTCCTTCCAAAATGGGTTC 834
QY 841 TTCTGCGATCAGAAAGCCAGTGTCTCACCAGAGAGGACCTGGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATCTGTAGTCTTTCACAAAGGGAACATGTTGAACCTGTAGAGCC 894
QY 901 AGAAGCTAGCCAGTGGCTGTGCTCTCCTGAGTGTCTTTGCCATTTGCTGGGCTCCG 960
Db 895 AGGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTGCTGGGCTCCA 954
QY 961 TATTGCTGTTCATATGTTCTTTTCAATCTTATCGCAGAGGGAGCGCCCAATCGATT 1020
Db 955 TATTCTGTTCATATGTTCTTTTCAATTTTATTTTCTCAGCAACAGGTCCTAAATCAGTT 1014
QY 1021 TGGTACAGCATAGCTTTGGCTACAGTGGTTCAATTCATTTAATCCCTTTCTATAC 1080
Db 1015 TGGTATAGAAATGCAATTTGGCTTCAGTGGTTCAATTTCTTGTCAATCTCTTTGTAT 1074
QY 1081 CCTTTGTCACAGAGCTTTCCAGAGGCTTTCTGGAAGATCTCTGTGTGACAAAGCAA 1140
Db 1075 CCATTGTGTACAGGCTTTCAAAGGCTTTCTTGAANATATTTGTATAAAGGCAA 1134
QY 1141 CCAGCACCTTC---ACAGACCCAGTCAATCTTCTTGA 1176
Db 1135 CCTCTACCATCAACACACAGTCCGTGAGTATCTTCTTAA 1173
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RESULT 2

US-09-812-216-1

; Sequence 1, Application US/09812216

; Patent No. 6613533

; GENERAL INFORMATION:

; APPLICANT: Behan, Jiang Xu

; APPLICANT: Hedrick, Joseph A.

; APPLICANT: Laz, Thomas M.

; APPLICANT: Monsma, Frederick J. Jr.

; APPLICANT: Morse, Kelley L.

; APPLICANT: Umland, Shelby P.

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; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-812-216-1
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Query Match 56.9%; Score 669; DB 3; Length 1173;

Best Local Similarity 74.2%; Pred. No. 6.3e-218;

Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

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QY 1 ATGTGGAGTCTAAAGGCACTGACGTCCTTGGCACTGCTCAAGTCCCTTGGCATTT 60
Db 1 ATGCCAGATCTAATAGCACAAATCAATTTATCCTAAGCACTCGTGTACTTTAGCATTT 60
QY 61 TTAATGTCCTGCTGCTTTTGTCTATPAACGATAGGCAATGCTGTGTGTCATTTTAGCCTTT 120
Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCAATTTTAGCTTTT 120
QY 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCT 180
Db 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAACCTTGGCCATCTCT 180
QY 181 GACTTCTCTGGGTGCTCATCTCCATTTCTGTGTACATCCCTCACACGCTGTTTAACTGG 240
Db 181 GACTTCTTTGGGTGTGATCTCCATTCCTTTGTGATCATCCCTCACACGCTGTTGCAATGG 240
QY 241 AATTTTGGAAAGTGGAACTGTCATGTTTGGCTCATTTACTGACTATCTTTTGTGCAAGCA 300
Db 241 GAATTTTGGAAAGGAAATCTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
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Db 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATCGATACCTGTCAGTCTCAAAATGCTGTG 360
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QY 841 TTCTGCGATCAGAAAGCCAGTGTCTCACCAGAGAGGACCTGGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATCTGTAGTCTTTCACAAAGGGAACATGTTGAACCTGTAGAGCC 894
QY 901 AGAAGCTAGCCAGTGGCTGTGCTCTCCTGAGTGTCTTTGCCATTTGCTGGGCTCCG 960
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Db 955 TATTCTGTTCATATGTTCTTTTCAATTTTATTTTCTCAGCAACAGGTCCTAAATCAGTT 1014
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Db 1075 CCATTGTGTACAGGCTTTCAAAGGCTTTCTTGAANATATTTGTATAAAGGCAA 1134
QY 1141 CCAGCACCTTC---ACAGACCCAGTCAATCTTCTTGA 1176
Db 1135 CCTCTACCATCAACACACAGTCCGTGAGTATCTTCTTAA 1173
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Db 1135 CCTTACCATCACACACAGTGGTCAAGTATCTTCTTAA 1173

RESULT 3

US-09-875-076-13
; Sequence 13, Application US/09875076
; Patent No. 6869776
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280

; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-076-13

Query Match 56.9%; Score 669; DB 3; Length 1173;
Best Local Similarity 74.2%; Pred. No. 6.3e-218; Mismatches 9; Gaps 2;
Matches 875; Conservative 0;

Qy 1 ATGTCGGAGTCTAAACGGCACTGACGCTCTTGCCCACTGACTGCTCAAGTCCCTTGGCAATTT 60
Db 1 ATGCCAGATACATAATAGCACAAATCAATTTATCAATAAGCACTCGTGTACTTTAGCAATTT 60
Qy 61 TTAATGTCCCTGCTTGTCTTTTGTCTATAACGATAGGCAATGCTGTGCTCATTTTAGCCTTT 120
Db 61 TTTATGTCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGCTCATTTTAGCTTTT 120
Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAAATATTTTCTTAATTTGGCTATTTCT 180
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Qy 181 GACTTCTTGTGGGTGTCTATCTCCATTCCTCTGTATACATCCCTCACAGCTGTTCGAATGG 240
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Qy 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCAATTAAGTACTGACTATCTTTTGTGACAGCA 300
Db 241 GATTTTGGAAAGGAAATCTGTGATTTTGGCTCCTCACTACTGACTATCTGTTATGTACAGCA 300
Qy 301 TCCGTCTACAGTATGCTCTCATTTAGCTACGATCGATACCAAGTCAGTTCCTCAAAACGCTGTG 360
Db 301 TCTGTATATACATGTTCTCTCATGCTATGATGATGATGATGATGATGATGATGATGATGATG 360
Qy 361 CGTTATAGAGCACAGCACACTGGCACTCTGAAATTTGTTGCTCAAAATGGTGGCTGTTGG 420
Db 361 TCTTATAGAACTCAACATACCTAGTGGGTCTTGAAGATTTGTTACTCTGATGGTGGCGTTGG 420
Qy 421 ATACTGGCTTTCTTGTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
Db 421 GTGCTGGCTTCTTGTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 476
Qy 481 ACCAACACAGAGAGTGGCGAGCTGGCTGTTGTTACTGAGTGGTACATCTCTCGCATTTACA 540
Db 477 --TGAAGGTAGTGAATGTAACCTGGATTTTTTTCGGAATGGTACATCTCTTGCATCACA 534
Qy 541 GCATTCTTGGAAATTTCTGCTCCCTGCTCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 600
Db 535 TCATTCTTGGAAATTTCTGCTCCCTGCTCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 594
Qy 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGTGCTTACGATGATGATGATGATGATGATGATGAT 660
Db 595 TGGAGCTGTGGAAGCGTGTATCATCTCAGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 654
Qy 661 ACCTCTTCCAGGGGCACTGGACACTCACGAGAACTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 720
Db 655 GTCTCTTCCAACTCTGTGGACACTCAATCAGAGGTAGACTATCTTCAAGAGAGATCTCTT 714
Qy 721 CCTGGATTAAAGGAACCCAGCGCATCTCTTCAATTCAGAAAGTCCACGAGAGAGAGAGAGT 780
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Qy	781	CTCCTGCTGTCTTAAAGCATCATGAGCGGTAGTATCATCGCCTTCAAAAGTGGTTC	840
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Qy	841	TTCTGCCGATCAGAAAAGCCCGAGTGCCTTACCAGAGAGAGACGCTGGAGCTTCTCAGAGGC	900
Db	835	TTCTCCCATCAGATTCTGTAGCTCTTCAACAAAGGGAACATGTTGAATCTCTTAGAGCC	894
Qy	901	AGGAAGCTTAGCCAGGTGCTAGCTGTCTCTCTGAGTGTCTTTTGCCATTTGTCTGGGCTCCG	960
Db	895	AGGAGATTAGCCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTCTTTGCTGGGCTCCA	954
Qy	961	TATTGCCCTGTTCAAAATGTTCTTTTCAACTTATCGCAGAGGGAGCGCCCAAAATCGATT	1020
Db	955	TATTCTCTGTTTCAAAATGTCTTTTCAATTTTATTTCTCTCAGCAAAGGTCCTTAATCAATT	1014
Qy	1021	TGGTACAGCATPAGCCTTTTGGCTACAGTGGTTCAATTTCACTTATTAATCCCTTCTATAC	1080
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Qy	1081	CTTTTGTGCCACAGACGTTTCCAGAAGCTTTCTGGGAAGTACTCTCTGTGCACAAAGCAA	1140
Db	1075	CCATTGTCACAAGCGCTTCAAAAGCCTTCTTGAATAATATTTTCTATAAAAAAGCAA	1134
Qy	1141	CCAGCACCTTC---ACAGACCCAGTCAGTATCTTCTTGA	1176
Db	1135	CCTCTACCATCAACAACAGTCGGTCAGTATCTTCTTAA	1173

RESULT 4

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US-09-891-053-2
? Sequence 2, Application US/09891053
? Patent No. 6750322
? GENERAL INFORMATION:
? APPLICANT: Itadani, Hiraku
? APPLICANT: Takimura, Tetsuo
? APPLICANT: Nakamura, Takao
? APPLICANT: Kobayashi, Masahiko
? APPLICANT: Tanaka, Ken-ichi
? APPLICANT: Hidaka, Yusuke
? APPLICANT: Ohta, Masaataka
? TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
? TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
? FILE REFERENCE: 06501-093001
? CURRENT APPLICATION NUMBER: US/09/891,053
? CURRENT FILING DATE: 2001-09-17
? PRIOR APPLICATION NUMBER: PCT/JP99/07280
? PRIOR FILING DATE: 1999-12-24
? PRIOR APPLICATION NUMBER: PCT/JP98/05967
? PRIOR FILING DATE: 1998-12-25
? PRIOR APPLICATION NUMBER: JP 11/145661
? PRIOR FILING DATE: 1999-05-25
? NUMBER OF SEQ ID NOS: 26
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 2
? LENGTH: 1239
? TYPE: DNA
? ORGANISM: Rattus norvegicus
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)...(1239)
US-09-891-053-2

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228	Db	CGCCATCTCGACATTCCTCGTGGGTGCTTCTGTCATCCCATTTGTACGTACCCATATGTGCT	287
231	Qy	GTTTAAAC---TGGAAATTTTGGAAAGTGAATCTGCATGTTTGGCTCAATTAAGTCAATCT	287
288	Db	GACCGGCGGTGTGGACCTTTCGGCGGGGCGCTTGAAGCTGTGGCTGTGTGTAGACTACCT	347
288	Qy	TTTGTGCACAGCATTCGCTCTACAGTATTTGCTCTCATTTAGCTTACGATCGATACAGTCACT	347
348	Db	ACTGTGTGCTCTCTCGCTCTTCAACATCGTACTCATCAGCTATGACCGATTCCTGTGCT	407
348	Qy	TTCAAAACGCTGTGCGTTTATAGACACAGCACTGGCATCTCTGAAATTTGTTGCTCAAT	407
408	Db	CACCTCGAGCTGTCTCTCACAGGGCCACAGAGGGGACACAGAGACGGGCCCTTTCGGAAGAT	467
408	Qy	GGTGGCTGTTTGGATATCTGGCTTTCTTGGTCAATGGGCCAATGATCTGGCTTCGGAT--	465
468	Db	GGCACTGGTGTGGGTGTGGCTTCTCTGTGTATGGGCTTGCCTCTGAGTTGGGAGTA	527
466	Qy	-----TCTTGAAGAACACAGCAACACAGAGGAGTGCAGCGCTGGCTTTGTTACTGAGTG	521
528	Db	CCTGTCTGTGGGCAAGTTCCATCCCGAGGGCCACTGCTATGCTGAGTTCTTCTACAACTG	587
522	Qy	GTACATCCTCGCANTTACAGATTTCTTGGAAATTCCTCTCCCTGCTCTCTTGGTGGTCTA	581
588	Db	GTACTTTTCTCATCACGGCCCTCCACCTCGAGTTCTTCAACGCCCTTCTCAGCGTTTACCTT	647
582	Qy	TTTTCAGTGTACAGATTTTACTTGGAGCCTGTGGAAAGCGTGGGAGTCTCAGTAGTGGCCCTAG	641
648	Db	CTTCAACCTCAGCATCTACCTGAACATCCAGAGGCGCACCCGCTTGTGATGGGGG	707
642	Qy	CCACGCTGGATTCATCGCTACTCTTCCAGGG----GCATGAGACATCTCAGCGAAACTG	697
708	Db	CCGTGAGGCTGGCCAGAACCCCAACAGATGCCAGCCCTCGCCACTCTCAGCTCCGCC	767
698	Qy	GGTTGGCTTGTAGGACAAAGTCTTCTTGATTTAAAGGAAACAGCGCGCATCCCTTCATTCAG	757
768	Db	CAGCTGTCTGGGCTGTGCGCCAAAGGGCATGGCGAGGCCATGCGTTCACAGCTCTGG	827
758	Qy	AAAGTCCACAGAGAAAGAGCAGTCTCTGTGTCTTAAAGGACTCAATGAGCGGTAGTA	817
828	Db	CAGCTCTCAAGGGGCACTGAGAGGCCACGCTCACTCAA--AAGGGGCTCCAAAGCCATCA	885
818	Qy	TCATCGCCTTCAAGTGGTTCCTTCTGCCGATCAGAAAGCCAGTGTCTTCCACAGAGAG	877
886	Db	GCATCTTTCAGCATCCCTGGAGAGCGCATGAGATGTTGTGCCAGAGCATCAC-----C	940
878	Qy	AGCACGTGGAGCTTCTCAGAGCGGAGAGCTAGCCAGGTCGTAGCTGTCTCTCTGAGTG	937
941	Db	AGCGCTTCGGCTGTGCGGGACAAAGAGGTGGCCAAAGTCCGCTGGCCATCATCGTGAGCA	1000
938	Qy	CTTTTGGCATTTGCTGGGCTCCGATTTGCTGTCTTTCACAAATGTTCTTTCAACTTATCGCA	997
1001	Db	TCTTTTGGGCTCTGCTGGGCGCCGTACACGCTCTCTAATGATCATCCGAGCTGTGTGCCATG	1060
998	Qy	GAGGGGAGCGCCCAATCGATTTGGTATCAGCATAGCCTTTTGGCTACAGTGGTTCAAATT	1057
1061	Db	GCCGCTGCATCCCGATT---ACTGGTACAGACGTCCTTCTGGCTTCTGTGGGCCAACT	1117
1058	Qy	CACTTATTAATCCCTTTCATATACCTTTTGTGCCACAGACGTTTCCAGAGAGGCTTTCGTGA	1117
1118	Db	CGGCGGTCAACCCCGTCTCTAGCCCACTGTGCCACTACAGCTTCCGACAGGCTTTCACCA	1177
1118	Qy	AGATACTCTG	1127
1178	Db	AGTCTCTCTG	1187

RESULT 5
US-09-891-053-5


```
; Sequence 5, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (351)...(1589)
; NAME/KEY: misc_feature
; LOCATION: (1)...(2700)
; OTHER INFORMATION: n = A,T,C or G
; US-09-891-053-5

Query Match      13.5%; Score 158.4; DB 3; Length 2700;
Best Local Similarity 50.6%; Pred. No. 8.4e-43;
Matches 551; Conservative 0; Mismatches 516; Indels 23; Gaps 6;

Qy 51 CTTGGCAATTTTAAATGTCCTGCTGCTTTTGGCTATACAGTAGGCAATGCTGTGTCAT 110
Db 458 CCTGGCTCGCTCATGGGCTGCTCATCGTGGCCACAGTAGTGGGCAACGGCTGGTCAT 517

Qy 111 TTATGCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTT 170
Db 518 GCTGCGCTTCTGGCGGATTCGAGCTCCGACCCAGAACAACTTCTTCTGCTCAACCT 577

Qy 171 GGCTATTTCTGACTTCTTGGTGGGTGTCATCTCCATCTCTGTACATCCCTCACAGCT 230
Db 578 CGCATCTCGACTTCTTGGGTGGCTTCTGATCCCATTTGATACCTCCCTATGTGCT 637

Qy 231 GTTTAAC---TGGAAATTTGGAAGTGAATCTGCATGTTTGGCTCAATTAAGTATCT 287
Db 638 GACCGCGGTGGACCTTGGCGGGGCTCTGCAAGCTGTGGCTGGGTAGACTACT 697

Qy 288 TTTGTGCACAGACTCCGCTACAGATATGTCCTCAATTAAGTACGATCGATACAGTCACT 347
Db 698 ACTGTGCTGCTCTCGCTCTTCAACATCGTACTCATCAGCTATGACCGAATTCCTGTGCT 757

Qy 348 TTCAAAAGCTGTGGTTATAGACACAGACACTGGCATCTGAAATTTGTCCTCAAT 407
Db 758 CACTCGAGCTGTCTCTACAGGGGCCAGAGGGGACACAGAGCGGGCGGTTCGGAAGAT 817

Qy 408 GGTGGCTTTTGGATCTAGCTTTCTTGGTCAATGGCCCAATGATCTGGCTTCGGAT-- 465
Db 818 GGCACTGGTGGGTGCTGGCTTCTGCTGTATGGGCTGCCATCTGAGTTGGAGTA 877

Qy 466 ----TCTTGGAAAGACAGCACCAACACAGAGGAGTGGAGCTGGCTTTGTTACTAGTG 521
Db 878 CCTGCTGGTGGCAGTTCCATCCCGAGGGGCCACTGCTATGCTGAGTTCTTCTCAACTG 937

Qy 522 GTACATCTCGCCATTTACAGATTTCTTGGAAATTCCTGCTCCCTGCTCTCTTGGTGTCTA 581
Db 522 GTACATCTCGCCATTTACAGATTTCTTGGAAATTCCTGCTCCCTGCTCTCTTGGTGTCTA 581

938 GTACTTTTCTCATCAGGCGCTCCACCCCTCGAGTTCTTCAOCCCTTCTCAGCGTTACCTT 997
582 TTTCACTGTACAGATTTTACTGGAGCCTGTGCGAAGCGTGGAGTCTCTAGTAGTGGCCCTAG 641
998 CTTCAACCTCAGCATCTACCTGAACATCCAGAGGCGCACCCGCTTCCGGCTTGTATGGGG 1057
642 CCACGCTGGATTCTATGCTACTCTTCCAGGG---GCACCTGGACACTCACGCGAGAACTG 697
1058 CGTGAAGCTGGCCAGAACCCCAACAGATGCCCAGCCTTCGCCACTCTCAGCTCCGCC 1117
698 GGTGGCTTTAGGACAAAGTCTTCTTGGATTTAAAGGAACGAGCGGCAATCCCTTCAATCAG 757
1118 CAGCTGCTGGGCTGCTGGCCAAAAGGCAATGGCGAGGCAATGCGGTTGCACAGCTCTGG 1177
758 AAAGTCCAGGAGGAAGAGCAGTCTCTCTGCTGCTTAAAGGACTCAATGAGCGGTAGTA 817
1178 CAGCTCCTCAAGGGGCACTGAGAGGCCACGCTCACTCAA--AAGGGGCTCCAGGCCATCA 1235
818 TCATCGCTTTCAAAGTGGGTCTCTTCTGCGGATCAGAAAGCCCAAGTCTTCCACGAGAG 877
1236 GCATCTTACGATCCCTGGAGAGCGCATGAAGTGTGTCCAGAGCATCACCC---C 1290
878 AGCAGCTGGAGCTTCTCAGAGGAGGAGTACGAGGTCGCTAGCTGTCTCTGAGTG 937
1291 AGCGCTTCCGGCTGTGCGGGACAAGAAAGGTGGCAAGTGGCTGGCCCATCATCGTAGCA 1350
938 CTTTGGCATTTGCTGGGCTCCGTTATTTGCTGCTGTTTCAATTTCTTCAACTTATCGCA 997
1351 TCTTGGGCTCTGCTGGGCGCGTACACGCTCTCTAATGATCATCCGAGCTGCTTGGCATG 1410
998 GAGGGAGCGCCCAATCGATTTGTTAGAGTAGAGCTTTTGGCTACAGTGGTTCATTT 1057
1411 GCGCTGCTATCCCCGATTT---ACTGGTACGAGAGCTCTTCTGCTTCTTGGGCCAACT 1467
1058 CACTTATTAATCCCTTTCTATATACCTTTTGTGCCACAGACGTTTCCAGAAGGCTTTCTGGA 1117
1468 CGCGCGTCAACCCGCTCTTACCCTAGTGGCCACTACAGCTTCCGAGAGGCTTTCACCA 1527
1118 AGATACCTTG 1127
1528 AGCTCCTCTG 1537

RESULT 6
US-08-985-090-3
; Sequence 3, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
```


QY 584 TCAGGTACAGATTACTGAGCGCTGTGGAGCGTGGAGTCTCAG 629
Db 650 TTAACCTCAGCATCTACCTGAACATCCAGAGCGCACCCGCTCCG 695

RESULT 8

US-09-167-354-6
; Sequence 6, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/167,354A
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-167-354-6

Query Match 11.8%; Score 138.4; DB 3; Length 1335;
Best Local Similarity 54.8%; Pred. No. 3.7e-36;
Matches 321; Conservative 0; Mismatches 256; Indels 9; Gaps 2;
QY 53 TGGCAATTTTAAATGTCCTGCTGCTTTTGGCTATACGATAGGAATGCTGCTCATTT 112
Db 110 TGGCGCGCTCATGGCGCTGCTCATCTGGCCACGGTGTGGGACGCGCTGTCATGC 169
QY 113 TAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGG 172
Db 170 TCGCCTTCGTGGCGGACTCGAGCCTCGGCACCCAGAACTTCTTCTGCTCAACCTCG 229
QY 173 CTATTTCTGACTTCTTCTGGGAGTGAATCTGCAATGTTTGGCTCATTAAGTATCTTT 289
Db 230 CCATCTCCGACTTCTCTGCTGGCGGCTTCTGCAATCCACTGTATGATACCTACGTCGA 289
QY 232 -TTTAACTGGAATTTTGGAGTGAATCTGCAATGTTTGGCTCATTAAGTATCTTT 289
Db 290 CAGGCGCTGGACCTTCTGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGGACTACCTGC 349
QY 290 TGTGCACAGCATCCGCTCAGATATTGCTCTCATTAAGTATGCTAGTGGCTGATGCTGCTCA 349
Db 290 TGTGCACAGCATCCGCTCAGATATTGCTCTCATTAAGTATGCTAGTGGCTGATGCTGCTCA 349
QY 350 TGTGCACCTCCTCTGCTTCAACATCGTGTCTATCAGCTACGACCGCTTCTCTGCTGCTCA 409
Db 350 CAAACGCTGTGCGTTATAGACACAGCACACTGGCATCTCTGAAATTTGTTGCTCAATGG 409
QY 410 CCGAGCGGCTCTCATACCGGGCCAGAGGGTGACACGGCGGGGAGTGGCGGAGATGC 469
Db 410 TGGCTGTTGGATGACTGGCTTTCTTGGTCAATGGCCAAATGATTTGGCTTCGGA----- 464
QY 470 TGTGTTGGTGGTGGCTTCTGCTGTGACGAGCGGCTGACACGGCGGGGAGTGGCGGAGTACC 529
Db 465 -TTCTTTGGAAGAACAGACACACAGAGGAGTGGAGGCTGGCTTTGTTACTGAGTGGT 523
QY 530 TGTTCGGGGGAGCTCCATCCCGAGGGCCACTGCTATGCGAGTTCCTTCTACAACTGGT 589
Db 524 ACATCTCGGCATTAAGCAATTTTGGAAATTTCTGCTCCCTGCTCTCTCTGGTGGTCTATT 583
QY 590 ACTTCTCATCAGCGCTTCCACCTGGAGTCTTTTACGCCCTTCTCTCAGGCTCACCTTCT 649
Db 584 TCAGTGTACAGATTACTGAGCGCTGTGGAAGCGTGGAGTCTCAG 629
QY 650 TTAACCTCAGCATCTACCTGAACATCCAGAGCGCACCCGCTCCG 695

RESULT 10

RESULT 9
US-09-642-855-6
; Sequence 6, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642,855
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-6

Query Match 11.8%; Score 138.4; DB 3; Length 1335;
Best Local Similarity 54.8%; Pred. No. 3.7e-36;
Matches 321; Conservative 0; Mismatches 256; Indels 9; Gaps 2;
QY 53 TGGCAATTTTAAATGTCCTGCTGCTTTTGGCTATACGATAGGAATGCTGCTCATTT 112
Db 110 TGGCGCGCTCATGGCGCTGCTCATCTGGCCACGGTGTGGGACGCGCTGTCATGC 169
QY 113 TAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGG 172
Db 170 TCGCCTTCGTGGCGGACTCGAGCCTCGGCACCCAGAACTTCTTCTGCTCAACCTCG 229
QY 173 CTATTTCTGACTTCTTCTGGGAGTGAATCTGCAATGTTTGGCTCATTAAGTATCTTT 289
Db 230 CCATCTCCGACTTCTCTGCTGGCGGCTTCTGCAATCCACTGTATGATACCTACGTCGA 289
QY 232 -TTTAACTGGAATTTTGGAGTGAATCTGCAATGTTTGGCTCATTAAGTATCTTT 289
Db 290 CAGGCGCTGGACCTTCTGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGGACTACCTGC 349
QY 290 TGTGCACAGCATCCGCTCAGATATTGCTCTCATTAAGTATGCTAGTGGCTGATGCTGCTCA 349
Db 350 TGTGCACCTCCTCTGCTTCAACATCGTGTCTATCAGCTACGACCGCTTCTCTGCTGCTCA 409
QY 350 CAAACGCTGTGCGTTATAGACACAGCACACTGGCATCTCTGAAATTTGTTGCTCAATGG 409
Db 410 CCGAGCGGCTCTCATACCGGGCCAGAGGGTGACACGGCGGGGAGTGGCGGAGATGC 469
QY 410 TGGCTGTTGGATGACTGGCTTTCTTGGTCAATGGCCAAATGATTTGGCTTCGGA----- 464
Db 470 TGTGTTGGTGGTGGCTTCTGCTGTGACGAGCGGCTGACACGGCGGGGAGTGGCGGAGTACC 529
QY 465 -TTCTTTGGAAGAACAGACACACAGAGGAGTGGAGGCTGGCTTTGTTACTGAGTGGT 523
Db 530 TGTTCGGGGGAGCTCCATCCCGAGGGCCACTGCTATGCGAGTTCCTTCTACAACTGGT 589
QY 524 ACATCTCGGCATTAAGCAATTTTGGAAATTTCTGCTCCCTGCTCTCTCTGGTGGTCTATT 583
Db 590 ACTTCTCATCAGCGCTTCCACCTGGAGTCTTTTACGCCCTTCTCTCAGGCTCACCTTCT 649
QY 584 TCAGTGTACAGATTACTGAGCGCTGTGGAAGCGTGGAGTCTCAG 629
Db 650 TTAACCTCAGCATCTACCTGAACATCCAGAGCGCACCCGCTCCG 695

US-09-642-514-6
; Sequence 6, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Brlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642,514
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-514-6

Query Match 11.8%; Score 138.4; DB 3; Length 1335;
Best Local Similarity 54.8%; Pred. No. 3.7e-36;
Matches 321; Conservative 0; Mismatches 256; Indels 9; Gaps 2;

QY 53 TGGCATTTTAAATGTCCTGCTGCTTTTGTCTATAACGATAGGCAATGCTGTGGTCATTT 112
DB 110 TGGCCGGCTCATGGCGCTCTCATCGTGGCCACGGTGTGGGCAACGGCTGGTCATGC 169
QY 113 TAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATTTTCTTAAATTTGG 172
DB 170 TCGCCTTCGTGGCGACTCGAGCTCCGCCACCCAGAACAACTTCTTCTGCTCAACTCG 229
QY 173 CTATTTCTGACTTCTTGTGGGTGTCATCTCCATTCTCTGTACATCCCTCACACGCTG- 231
DB 230 CCATCTCCGACTTCTCTGTCGGCGCTTCTGCACTCCACTGTATGTACCTACGTCGTA 289
QY 232 -TTTAACTGGAATTTTGGAACTGTGAATCTGCATGTTTGGCTCATTTACTGACTATCTTT 289
DB 290 CAGGCGCTGGGACTTTCGGCCGGGGCTCTGCAAGCTGTGGCTGGTAGTGACTACTGTC 349
QY 290 TGTGCACAGCATCCGCTTACAGTATTGTCTCTCAATTAGCTACGATCGATACCACTCAGTTT 349
DB 350 TGTGCACCTCTCTGCTTCAACATGCTCTCATCAGCTACGACCGCTTCTCTGTCGTCA 409
QY 350 CAAAACGCTGTGGTTATAGACACAGCACACCTGGGATCTCTGAAATTTGTCTCAATGG 409
DB 410 CCGAGCGGTCTCATACCGGGCCAGCAGGTGACACGCGGGCGGCGAGTGCAGGAGATGC 469
QY 410 TGGCTGTTTGGATACCTGGCTTCTTGGTCAATGGCCCAATGATTCTGGCTTCGGA---- 464
DB 470 TGTGTGTGGGTGCTGGGCTTCTCTGCTGTACGACAGCATCCCTGAGCTGGAGTACC 529
QY 465 -TTCTTGGAAAGACAGACACAAACACAGAGAGAGTGCAGGCTTGGCTTTGTACTAGTGGT 523
DB 530 TGTCCGGGGCAGCTCCATCCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACTGGT 589
QY 524 ACATCTCGCCATTACAGCATTTTGGAAATTTCTGCTCTCTGCTCTCTGCTGCTGCTATT 583
DB 590 ACTTCTCATACGGCTTCCACCTGGAGTTCTTTACGCCCTTCTTCTCAGGCTCACCTTCT 649
QY 584 TCAGTGTACAGATTTACTGGAGCTGTGGAAGCGTGGAGTCTCAG 629
DB 650 TTAACCTCAGCATCTACCTGAACATCCAGAGGGCGCACCCGCTCCG 695

RESULT 11
US-09-642-852-6
; Sequence 6, Application US/09642852

Patent No. 6855560
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Brlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642,852
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-852-6

Query Match 11.8%; Score 138.4; DB 3; Length 1335;
Best Local Similarity 54.8%; Pred. No. 3.7e-36;
Matches 321; Conservative 0; Mismatches 256; Indels 9; Gaps 2;

QY 53 TGGCATTTTAAATGTCCTGCTGCTTTTGTCTATAACGATAGGCAATGCTGTGGTCATTT 112
DB 110 TGGCCGGCTCATGGCGCTCTCATCGTGGCCACGGTGTGGGCAACGGCTGGTCATGC 169
QY 113 TAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATTTTCTTAAATTTGG 172
DB 170 TCGCCTTCGTGGCGACTCGAGCTCCGCCACCCAGAACAACTTCTTCTGCTCAACTCG 229
QY 173 CTATTTCTGACTTCTTGTGGGTGTCATCTCCATTCTCTGTACATCCCTCACACGCTG- 231
DB 230 CCATCTCCGACTTCTCTGTCGGCGCTTCTGCACTCCACTGTATGTACCTACGTCGTA 289
QY 232 -TTTAACTGGAATTTTGGAACTGTGAATCTGCATGTTTGGCTCATTTACTGACTATCTTT 289
DB 290 CAGGCGCTGGGACTTTCGGCCGGGGCTCTGCAAGCTGTGGCTGGTAGTGACTACTGTC 349
QY 290 TGTGCACAGCATCCGCTTACAGTATTGTCTCTCAATTAGCTACGATCGATACCACTCAGTTT 349
DB 350 TGTGCACCTCTCTGCTTCAACATGCTCTCATCAGCTACGACCGCTTCTCTGTCGTCA 409
QY 350 CAAAACGCTGTGGTTATAGACACAGCACACCTGGGATCTCTGAAATTTGTCTCAATGG 409
DB 410 CCGAGCGGTCTCATACCGGGCCAGCAGGTGACACGCGGGCGGCGAGTGCAGGAGATGC 469
QY 410 TGGCTGTTTGGATACCTGGCTTCTTGGTCAATGGCCCAATGATTCTGGCTTCGGA---- 464
DB 470 TGTGTGTGGGTGCTGGGCTTCTCTGCTGTACGACAGCATCCCTGAGCTGGAGTACC 529
QY 465 -TTCTTGGAAAGACAGACACAAACACAGAGAGAGTGCAGGCTTGGCTTTGTACTAGTGGT 523
DB 530 TGTCCGGGGCAGCTCCATCCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACTGGT 589
QY 524 ACATCTCGCCATTACAGCATTTTGGAAATTTCTGCTCTCTGCTCTCTGCTGCTGCTATT 583
DB 590 ACTTCTCATACGGCTTCCACCTGGAGTTCTTTACGCCCTTCTTCTCAGGCTCACCTTCT 649
QY 584 TCAGTGTACAGATTTACTGGAGCTGTGGAAGCGTGGAGTCTCAG 629
DB 650 TTAACCTCAGCATCTACCTGAACATCCAGAGGGCGCACCCGCTCCG 695

RESULT 12
US-09-891-053-21
; Sequence 21, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:

APPLICANT: Itadani, Hiraku
APPLICANT: Takimura, Tetsuo
APPLICANT: Nakamura, Takao
APPLICANT: Kobayashi, Masahiko
APPLICANT: Tanaka, Ken-ichi
APPLICANT: Hidaka, Yusuke
APPLICANT: Ohta, Masataka
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
FILE REFERENCE: 06501-083001
CURRENT APPLICATION NUMBER: US/09/891.053
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: PCT/JP99/07280
PRIOR FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: PCT/JP98/05967
PRIOR FILING DATE: 1998-12-25
PRIOR APPLICATION NUMBER: JP 11/145661
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 2050
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (271)....(1629)
US-09-891-053-21

Query Match 11.8%; Score 138.4; DB 3; Length 2050;
Best Local Similarity 54.8%; Pred. No. 4.9e-36;
Matches 321; Conservative 0; Mismatches 256; Indels 9; Gaps 2;
QY 53 TGGCAATTTTAAAGTCCCTGCTGCTTTTGGCTATACGATAGGCAATGCTGTGTCATTT 112
DB 380 TGGCCGGCTCATGGCGCTGCTCATGCTGGCCAGGCTGGGCAACGCGTGTGTCATGC 439
QY 113 TAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGG 172
DB 440 TCGCCTTGTGGCGGACTCGAGCCTCCGCCACCCAGAACAACTTCTTCTGCTCAACCTG 499
QY 173 CTATTTCTGACTTCTTCTGGGTGTCATCTCCATTCCTGTATACATCCCTCACACGCTG- 231
DB 500 CCATCTCCGACTTCTCTGTCGGCCCTTGTGATCCCACTGTATGATACCTACCTGCTGA 559
QY 232 --TTTAACTGGAATTTTGGAGTGGAACTGCTATGTTTGGCTCATTAAGTACTATCTTT 289
DB 560 CAGCCGCTGGACCTTCGGCCGGGCTCTGCAAGCTGTGGCTGTAGTGAAGTACTCTGC 619
QY 290 TGTGCAAGCATCCGCTCAAGTATTCCTCATTAAGTACGATCGATACGATCAAGTCACTTT 349
DB 620 TGTGCACTCTCTGCTTCAACATCTGCTCATCAGTACGACGCGCTTCTGTGCTGCA 679
QY 350 CAAACGCTGCGTTATAGAGCAGACACACTGCGATCTCGAAATTTGTTGCTCAATGG 409
DB 680 CCGAGCGGTCTCATACCGGGCCAGCAGGGTGACACGCGCGGGGAGTGGGAGATGC 739
QY 410 TGGCTGTTGGATCTGGCTTTCTTGGTCAATGCGCCCAATGATCTGGCTTCGGA----- 464
DB 740 TGTGTTGTTGGTGTGGCTTCTTGTGTGTAAGACCAAGCCATCCCTGAGCTGGAGTACC 799
QY 465 -TTCTTGGAAAGACAGACCAACACAGAGAGTGGAGCTGGCTTTGTTACTGAGTGGT 523
DB 800 TGTCCGGGGGAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTCTTCTTACAACTGGT 859
QY 524 ACATCTCGGCATTTACAGCATTTTGGAAATCTGCTCCCTGCTCTCTGCTGCTTATT 583
DB 860 ACTTCTCATCAGGGCTTCACCCCTGGAGTCTTTTACGCCCTTCTCAGGCTCACCTTCT 919
QY 584 TCAGTGTACAGATTTACTGAGGCTGTGGAGGCTGGAGTGTCTCAG 629
DB 920 TTAACCTCAGCATCTACCTGAAACATCCAGAGGGCGACCCCGCTCCG 965

RESULT 14
US-08-985-090-1

RESULT 13
US-09-949-016-5059
Sequence 5059, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949.016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5059
LENGTH: 2665
TYPE: DNA
ORGANISM: Human
US-09-949-016-5059

Query Match 11.8%; Score 138.4; DB 3; Length 2665;
Best Local Similarity 54.8%; Pred. No. 5.9e-36;
Matches 321; Conservative 0; Mismatches 256; Indels 9; Gaps 2;
QY 53 TGGCAATTTTAAAGTCCCTGCTGCTTTTGGCTATACGATAGGCAATGCTGTGTCATTT 112
DB 401 TGGCCGGCTCATGGCGCTGCTCATGCTGGCCAGGCTGGGCAACGCGTGTGTCATGC 460
QY 113 TAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGG 172
DB 461 TCGCCTTGTGGCGGACTCGAGCCTCCGCCACCCAGAACAACTTCTTCTGCTCAACCTG 520
QY 173 CTATTTCTGACTTCTTCTGGGTGTCATCTCCATTCCTGTATACATCCCTCACACGCTG- 231
DB 521 CCATCTCCGACTTCTCTGTCGGCCCTTGTGATCCCACTGTATGATACCTACCTGCTGA 580
QY 232 --TTTAACTGGAATTTTGGAGTGGAACTGCTATGTTTGGCTCATTAAGTACTATCTTT 289
DB 581 CAGCCGCTGGACCTTCGGCCGGGCTCTGCAAGCTGTGGCTGTAGTGAAGTACTCTGC 640
QY 290 TGTGCAAGCATCCGCTCAAGTATTCCTCATTAAGTACGATCGATACGATCAAGTCACTTT 349
DB 641 TGTGCACTCTCTTGGCTTCAACATCTGCTCATCAGTACGACGCGCTTCTGTGCTGCA 700
QY 350 CAAACGCTGCGTTATAGAGCAGACACACTGCGATCTCGAAATTTGTTGCTCAAAATGG 409
DB 701 CCGAGCGGTCTCATACCGGGCCAGCAGGGTGACACGCGCGGGGAGTGGGAGATGC 760
QY 410 TGGCTGTTGGATCTGGCTTTCTTGGTCAATGCGCCCAATGATCTGGCTTCGGA----- 464
DB 761 TGTGTTGTTGGTGTGGCTTCTTGGCTTCTGTAACGACAGCCATCTCTGAGTGGAGTACC 820
QY 465 -TTCTTGGAAAGACAGACCAACACAGAGAGTGGAGCTGGCTTTGTTACTGAGTGGT 523
DB 821 TGTCCGGGGGAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTCTTCTTACAACTGGT 880
QY 524 ACATCTCGGCATTTACAGCATTTTGGAAATCTGCTCCCTGCTCTCTGCTGCTTATT 583
DB 881 ACTTCTCATCAGGGCTTCACCCCTGGAGTCTTTTACGCCCTTCTCAGGCTCACCTTCT 940
QY 584 TCAGTGTACAGATTTACTGAGGCTGTGGAGGCTGGAGTGTCTCAG 629
DB 941 TTAACCTCAGCATCTACCTGAAACATCCAGAGGGCGACCCCGCTCCG 986

; Sequence 1, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
US-08-985-090-1

Query Match 11.8%; Score 138.4; DB 2; Length 2689;
Best Local Similarity 54.8%; Pred. No. 5.9e-36;
Matches 321; Conservative 0; Mismatches 256; Indels 9; Gaps 2;

QY 53 TGGCATTTTTAAATGTCCTGCTTTTGGCTATAAGCATAGGCAATGCTGGTCAATTT 112
DB 400 TGGCCGGCTCATGGCGCTGCTCATCGTGCCACGGTGTGGGCAAGCGCTGTCATGC 459

QY 113 TAGCCTTTGTAGCAGACAGAACTTAGACATCGAAGTAATTTTCTTAAATTTGG 172
DB 460 TCGCCTTCGTGGCGACTCGAGCTCGCGACCCAGAACAACTTCTTCTGCTCAACCTCG 519

QY 173 CTATTTCTGACTTCTGCTGGGTGTCATCTCCATCTCTGTATACCCCTCACACGCTG- 231
DB 520 CCATCTCCGACTTCTGCTGGCGCCTTCTGCATCCACCTGTATGACCTCTAGTCTGA 579

QY 232 -TTTAACTGGAATTTTGGAAATGGAATCTGCAATGTTTGGCTCATTTACTGACTATCTTT 289
DB 580 CAGGCCGCTGAGCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGACTACTGTCG 639

QY 290 TGTGCACAGATCCGCTCAGATTTAGTTCCTCATTTAGCTACGATCGAATACAGTCAATTT 349
DB 640 TGTGCACCTCTCTGCTTCAACATCGTGTCTCATGACTACGACCGCTTCTGTCGCTCA 699

QY 350 CAAACGCTGCGCTTAGAGCAGACACACTGCACTCCCGAATTTGTTGCTCAAAATGG 409
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QY 410 TGGCTGTTGGATGACTGGCTTTCTTGGTCAATGCCCAATGATTTCTGGCTTCGGA----- 464

DB 760 TGCTGGTGTGGGTGCTGGCCTTCTGCTGTACGGACCAAGCATCTCTGAGCTGGAGTACC 819
QY 465 -TTCCTTGGAGAACAGCACCAACACAGAGAGAGTGGAGCTGCTTTTACTGAGTGGT 523
DB 820 TGTCCGGGGGAGCTCCATCCCGAGGGCCACTGCTATGCGAGTTCTTCTACAATGGT 879
QY 524 ACATCCTCGCCATTTACAGCAATTTTGGAAATTCCTGCTCCCTGCTCTCTTGGTGGTCTATT 583
DB 880 ACTTCTCATACGGCTTCCACCTGGAGTTCTTTAGCGCCTTCTCCTCAGGTCACCTTCT 939
QY 584 TCAGTGTACAGATTTACTGAGCCTGTGAAGGTGGAGTCTCAG 629
DB 940 TTAACCTCAGCATCTACTGAAACATCCAGAGGGCGACCCGCTCCG 985

RESULT 15
US-09-165-543-1
; Sequence 1, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
US-09-165-543-1

Query Match 11.8%; Score 138.4; DB 3; Length 2689;
Best Local Similarity 54.8%; Pred. No. 5.9e-36;
Matches 321; Conservative 0; Mismatches 256; Indels 9; Gaps 2;

QY 53 TGGCATTTTTAAATGTCCTGCTTTTGGCTATAAGCATAGGCAATGCTGGTCAATTT 112
DB 400 TGGCCGGCTCATGGCGCTGCTCATCGTGCCACGGTGTGGGCAAGCGCTGTCATGC 459

QY 113 TAGCCTTTGTAGCAGACAGAACTTAGACATCGAAGTAATTTTCTTAAATTTGG 172
DB 460 TGGCCTTCGTGGCGGACTCGAGCCTCCGACCCAGAACAACTTCTTCTGCTCAACCTCG 519

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Qy	232	--TTTAACTGGAATTTTGGAGTGAATCTGCATGTTTGGCTCATTTACTGACTATCTTT	289
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Qy	290	TGTGCACAGCATCCGTCCTACAGTATTTGCTCTCATTTAGTAGGATCGATACCA	349
Db	640	TGTGCACCTCCTCTGCGCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCCTGT	699
Qy	350	CARACGCTGTGCGTTATAGACACAGCACACTGGCATCCTGAAATTTGTTGCTCAAATGG	409
Db	700	CCCGAGCGTCTCATACCGGGCCACGAGGGTGAACGGCGGGGAGTGGGGAAGATGC	759
Qy	410	TGGCTGTTTGGATACTGGCTTTCTTTGGTCAATGGCCCAATGATTCCTGGCTTCGGA	464
Db	760	TGCTGGTGTGGTGTGGCTTTCCTGTGTACGGACCAAGCCATCCTGAGCTGGGAGTACC	819
Qy	465	-TTCTTGGAGAAACAGCACCAACACAGAGGAGTGGAGCCTGGCTTTGTTACTGAGTGGT	523
Db	820	TGTCGGGGGCGAGCTCCATCCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACTGGT	879
Qy	524	ACATCCTCGGCATTACAGCATTCCTTGGAAATTCCTGCTCCCTGTCTCTTGGTGGTCTATT	583
Db	880	ACTTCCCTCATACGGCTTCCACCTGGAGTTCTTTACGCCCTTCTCAGCGCTCACCTTCT	939
Qy	584	TCAGTGTACAGATTTACTGGAGCCTGTGGAGCGTGGGAGTCTCAG	629
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Search completed: April 29, 2006, 00:47:53
Job time : 257 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2006, 23:38:17 ; Search time 1113 Seconds
(without alignments)
8737.456 Million cell updates/sec

Title: US-10-626-126-6
Perfect score: 1176
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main.*
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2: /cgm2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
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9: /cgm2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgm2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1176	100.0	1176	8	US-10-626-445-6
2	1176	100.0	1176	9	US-10-626-126-6
3	1176	100.0	1176	9	US-10-626-398-6
4	958.4	81.5	1176	8	US-10-626-445-5
5	958.4	81.5	1176	9	US-10-626-126-5
6	958.4	81.5	1176	9	US-10-626-398-5
7	669	56.9	1173	3	US-09-812-216-1
8	669	56.9	1173	3	US-09-910-411-1
9	669	56.9	1173	3	US-09-875-076-13
10	669	56.9	1173	3	US-09-876-252-13
11	669	56.9	1173	3	US-10-052-193-1
12	669	56.9	1173	6	US-10-290-078-26
13	669	56.9	1173	6	US-10-273-983-13
14	669	56.9	1173	6	US-10-354-769-1
15	669	56.9	1173	6	US-10-393-807-13
16	669	56.9	1173	6	US-10-417-820A-13
17	669	56.9	1173	7	US-10-349-253A-1
18	669	56.9	1173	7	US-10-723-955-13
19	669	56.9	1173	7	US-10-782-596-13
20	669	56.9	1173	7	US-10-737-619-1
21	669	56.9	1173	8	US-10-626-445-1
22	669	56.9	1173	9	US-10-616-088-1
23	669	56.9	1173	9	US-10-626-126-1

24	669	56.9	1173	9	US-10-626-398-1	Sequence 1, Appli
25	669	56.9	1173	9	US-10-723-955-13	Sequence 13, Appl
26	669	56.9	1265	6	US-10-290-078-25	Sequence 25, Appl
27	669	56.9	1265	9	US-10-488-421-5	Sequence 5, Appli
28	669	56.9	1266	3	US-09-891-138A-5	Sequence 5, Appli
29	669	56.9	1300	3	US-09-852-165-1	Sequence 1, Appli
30	669	56.9	1300	7	US-10-696-673-1	Sequence 1, Appli
31	669	56.9	3689	5	US-10-225-567A-628	Sequence 628, App
32	669	56.9	3689	8	US-10-584-206-19	Sequence 19, Appl
33	669	56.9	3689	9	US-10-756-149-32	Sequence 32, Appl
34	668	56.8	1170	9	US-10-488-421-7	Sequence 7, Appli
35	616.8	52.4	1170	8	US-10-626-445-7	Sequence 7, Appli
36	616.8	52.4	1170	9	US-10-626-126-7	Sequence 7, Appli
37	616.8	52.4	1170	9	US-10-626-398-7	Sequence 7, Appli
38	494.6	42.1	1166	9	US-10-488-421-3	Sequence 3, Appli
39	422.2	35.9	1103	9	US-10-488-421-1	Sequence 1, Appli
40	268.4	22.8	1326	7	US-10-398-036-19	Sequence 19, Appl
41	158.4	13.5	1239	3	US-09-891-053-2	Sequence 2, Appli
42	158.4	13.5	1239	8	US-10-759-463-2	Sequence 2, Appli
43	158.4	13.5	2700	3	US-09-891-053-5	Sequence 5, Appli
44	158.4	13.5	2700	8	US-10-759-463-5	Sequence 5, Appli
45	153	13.0	1311	9	US-10-495-679A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-626-445-6
; Sequence 6, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; PRIOR FILING DATE: 2003-07-23
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-445-6

Query Match	100.0%;	Score 1176;	DB 8;	Length 1176;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1176;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGTCGGAGTCTAACGGCAGCTGCTTGGCAGTCACTGCTCAAGTCCCTTGGCATTTT	60	
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Qy	61	TTAATGTCCTGCTTGTCTTGTATACGATGCAATGCTGTGTCATTTTAGCCCTTTT	120	
Db	61	TTAATGTCCTGCTTGTCTTGTATACGATGCAATGCTGTGTCATTTTAGCCCTTTT	120	
Qy	121	GTACGACAGAAACCTTAGACATCGAAGTAATATTTTTTTTCTTAATTTGGCTATTTCCT	180	
Db	121	GTACGACAGAAACCTTAGACATCGAAGTAATATTTTTTTTCTTAATTTGGCTATTTCCT	180	
Qy	181	GACTTCTTGGGTGTCATCTCAATTCCTCTGTACATCCCTCACAGCTGTTAACTGG	240	
Db	181	GACTTCTTGGGTGTCATCTCAATTCCTCTGTACATCCCTCACAGCTGTTAACTGG	240	
Qy	241	AATTTTGGAGTGAATCTGCATGTTTTGGCTCAATTAATCTTTTGTGCACAGCA	300	
Db	241	AATTTTGGAGTGAATCTGCATGTTTTGGCTCAATTAATCTTTTGTGCACAGCA	300	

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361 CGTTATAGACACAGACACTGCGATCCTGAAATTTGTTCTCAAAATGTTGGTGTG 420
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481 ACCAACACAGAGAGTGCAGCTGCTGTTGTTACTGAGTGTACATCCTCGCCATTACA 540
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541 GCATTTCTGGAAATTCCTGCTCCCTGTCCTCTGTTGGTGTCTATTTCAAGTGTACAGATTTAC 600
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601 TGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTAGCCACAGCTGGATTCATCGCT 660
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661 ACCTCTTCCAGGGGCACTGACACTCACGCAGAACTGGGTTGGTGTAGGACAAAGTCTT 720
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1021 TGCTACAGCATAGCTTTTGGCTACAGTGTTCATTTCAATTAATCCCTTTCTATAC 1080
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1141 CCAGCACCTTTCACAGACCCAGTCAAGTATCTTCTTGA 1176

RESULT 2
US-10-626-126-6
; Sequence 6, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23

; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-126-6

Query Match 100.0%; Score 1176; DB 9; Length 1176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCGAGTCTAAACGGCACTGACGCTTGGCACTGACTGCTCAAGTCCCTTGGCATTT 60
DB 1 ATGTCGAGTCTAAACGGCACTGACGCTTGGCACTGACTGCTCAAGTCCCTTGGCATTT 60
QY 61 TTAATGTCCTGCTTGTCTAATACGATAGGCAATGCTGTGCTCAATTTTGTAGCTTT 120
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QY 181 GACTTCTTGGGTTGTCATCTCCATCTCTGTGTACATCCCTCACACGCTGTTAACTGG 240
DB 181 GACTTCTTGGGTTGTCATCTCCATCTCTGTGTACATCCCTCACACGCTGTTAACTGG 240
QY 241 AATTTTGGAGTGGATCTGCAATGTTTGGCTCAATTTACTGACTATCTTTTGTGCACAGCA 300
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DB 361 CGTTATAGAGCAAGACACTGCGATCTTGAAAAATTTGTTGCTCAAAATGTTGGTGTG 420
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Db      841  |||||TTCTGCCGATCAGAAAGCCAGTGCCTTCAACAGAGAGAGACGTGGAGCTTCTCAGAGGC 900
Qy      901  AGGAAGCTAGCCAGGTGCGTAGCTGCTCCTCTGAGTGTCTTTGCCCAATTTGCTGGGCTCCG 960
Db      901  AGGAAGCTAGCCAGGTGCGTAGCTGCTCCTCTGAGTGTCTTTGCCCAATTTGCTGGGCTCCG 960
Qy      961  TATTGCTGTTCACAAATGTTCTTCAACTATCGCAGAGGGGAGCGCCCCCAATCGAATT 1020
Db      961  TATTGCTGTTCACAAATGTTCTTCAACTATCGCAGAGGGGAGCGCCCCCAATCGAATT 1020
Qy      1021  TGGTACAGCATAGCTTTTGGCTACAGTGGTTCAATTCACCTATTAATCCCTTTCTATAC 1080
Db      1021  TGGTACAGCATAGCTTTTGGCTACAGTGGTTCAATTCACCTATTAATCCCTTTCTATAC 1080
Qy      1081  CTTTGTGCCACAGAGCTTTCCAGAGGCTTTCTGGAAGATACCTGTGTGACAAAGCAA 1140
Db      1081  CTTTGTGCCACAGAGCTTTCCAGAGGCTTTCTGGAAGATACCTGTGTGACAAAGCAA 1140
Qy      1141  CCAGCACCTTTCACAGAGCCAGTCAGTATCTTCTTGA 1176
Db      1141  CCAGCACCTTTCACAGAGCCAGTCAGTATCTTCTTGA 1176

RESULT 3
US-10-626-398-6
; Sequence 6, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-398-6

Query Match      100.0%; Score 1176; DB 9; Length 1176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGTGGAGTCTAACGGCACTGAGCTCTTGCCACTGACTGCTCAAGTCCCTTTGGCAATTT 60
Db      1  ATGTGGAGTCTAACGGCACTGAGCTCTTGCCACTGACTGCTCAAGTCCCTTTGGCAATTT 60
Qy      61  TTAATGTCCTGTGCTTTGCTATTAACGATAGGCAATGCTGTGGTCAATTTAGCCCTTT 120
Db      61  TTAATGTCCTGTGCTTTGCTATTAACGATAGGCAATGCTGTGGTCAATTTAGCCCTTT 120
Qy      121  GTAGCAGACAGAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 180
Db      121  GTAGCAGACAGAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 180
Qy      181  GACTTCTTCTGGGTGTCAATCCATTCCTCTGTACATCCCTCACAGCTGTTTAACCTGG 240
Db      181  GACTTCTTCTGGGTGTCAATCCATTCCTCTGTACATCCCTCACAGCTGTTTAACCTGG 240
Qy      241  AATTTTGAAGTGAATCTGATGTTTGGCTCATTAATGACTATCTTTTGTGCACAGCA 300
Db      241  AATTTTGAAGTGAATCTGATGTTTGGCTCATTAATGACTATCTTTTGTGCACAGCA 300
Qy      301  TCGTCTACAGTATTGCTCATTAATGACTATCGATACAGTCAGTTCAGAGCGTGTG 360
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Db      301  TCGTCTACAGTATTGCTCATTAATGACTATCGATACGATCAGTTCAGTTCAAACGCTGTG 360
Qy      361  CGTTATAGAGCACAGACACTGGCATCTCGAAAATTTGTTGCTCAAAATGGTGGCTTTGG 420
Db      361  CGTTATAGAGCACAGACACTGGCATCTCGAAAATTTGTTGCTCAAAATGGTGGCTTTGG 420
Qy      421  ATACTGGCTTTCTTTGGTCAATGATTCGCTTCGGATTCTTCGAAAGAACAGC 480
Db      421  ATACTGGCTTTCTTTGGTCAATGATTCGCTTCGGATTCTTCGAAAGAACAGC 480
Qy      481  ACCAACACAGAGAGAGTGGAGCTTGGTTTACTGAGTGGTACATCTCTCGCCATTTACA 540
Db      481  ACCAACACAGAGAGAGTGGAGCTTGGTTTACTGAGTGGTACATCTCTCGCCATTTACA 540
Qy      541  GCATTTCTGGAATTCCTGCTCCCTGCTCTCTGGTGGTCTATTTTCAGTGTACAGATTAC 600
Db      541  GCATTTCTGGAATTCCTGCTCCCTGCTCTCTGGTGGTCTATTTTCAGTGTACAGATTAC 600
Qy      601  TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTAGCCAGCCAGCTGGAATTCATCGCT 660
Db      601  TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTAGCCAGCCAGCTGGAATTCATCGCT 660
Qy      661  ACCTCTTCCAGGGGCACTGGACACTCAACGAGAACTGGGTGGCTTGTAGGACAAAGTCTT 720
Db      661  ACCTCTTCCAGGGGCACTGGACACTCAACGAGAACTGGGTGGCTTGTAGGACAAAGTCTT 720
Qy      721  CTTGGAATTAAGGAACAGCCGATCCTCTTCAATTCAGAAAGTCCACGAGAAAGAGCAGT 780
Db      721  CTTGGAATTAAGGAACAGCCGATCCTCTTCAATTCAGAAAGTCCACGAGAAAGAGCAGT 780
Qy      781  CTCCTGGTGTCTTAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
Db      781  CTCCTGGTGTCTTAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
Qy      841  TTCTGCGCATCAGAAAGCCAGTGTCTTCAACAGAGAGAGCACGCTGGAGCTTCTCAGAGGC 900
Db      841  TTCTGCGCATCAGAAAGCCAGTGTCTTCAACAGAGAGAGCACGCTGGAGCTTCTCAGAGGC 900
Qy      901  AGGAAGCTAGCCAGGTGCGTAGCTGCTCCTGAGTGTCTTTGCCAATTTGCTGGGCTCCG 960
Db      901  AGGAAGCTAGCCAGGTGCGTAGCTGCTCCTGAGTGTCTTTGCCAATTTGCTGGGCTCCG 960
Qy      961  TATTGCTGTTCACAAATGTTCTTCAACTATCGCAGAGGGGAGCGCCCCCAATCGAATT 1020
Db      961  TATTGCTGTTCACAAATGTTCTTCAACTATCGCAGAGGGGAGCGCCCCCAATCGAATT 1020
Qy      1021  TGGTACAGCATAGCTTTTGGCTACAGTGGTTCAATTCACCTATTAATCCCTTTCTATAC 1080
Db      1021  TGGTACAGCATAGCTTTTGGCTACAGTGGTTCAATTCACCTATTAATCCCTTTCTATAC 1080
Qy      1081  CTTTGTGCCACAGAGCTTTCCAGAGGCTTTCTGGAAGATACCTGTGTGACAAAGCAA 1140
Db      1081  CTTTGTGCCACAGAGCTTTCCAGAGGCTTTCTGGAAGATACCTGTGTGACAAAGCAA 1140
Qy      1141  CCAGCACCTTTCACAGAGCCAGTCAGTATCTTCTTGA 1176
Db      1141  CCAGCACCTTTCACAGAGCCAGTCAGTATCTTCTTGA 1176
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RESULT 4

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US-10-626-445-5
; Sequence 5, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
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; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-445-5

Query Match      81.5%; Score 958.4; DB 8; Length 1176;
Best Local Similarity 88.4%; Pred. No. 6.4e-295;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 1 ATGTGGAGTCTAAGCGCACTGACGCTTGGCCACTGACTGCTCAAGTCCCTTGGCATTT 60
Db 1 ATGTGGAGTCTAAGCGCACTGACGCTTGGCCACTGACTGCTCAAGTCCCTTGGCATTT 60
QY 61 TTAATGTCCTGCTGCTCTTTTGGCTATACGATAGGCAATGCTGTGCTCAATTTAGCCTTT 120
Db 61 TTAATGTCCTGCTGCTCTTTTGGCTATACGATAGGCAATGCTGTGCTCAATTTAGCCTTT 120
QY 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCTT 180
Db 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCTT 180
QY 181 GACTTCTCTGTGGGTGTCATCTCCATCTCTGTATACATCCCTCACACGCTGTTAACTG 240
Db 181 GACTTCTCTGTGGGTGTCATCTCCATCTCTGTATACATCCCTCACACGCTGTTAACTG 240
QY 241 AATTTTGGAGTGGAAATCTGCATGTTTGGCTCATTAAGTACTATCTTTGTGCACAGCA 300
Db 241 AATTTTGGAGTGGAAATCTGCATGTTTGGCTCATTAAGTACTATCTTTGTGCACAGCA 300
QY 301 TCGCTCTACAGTATGTCCTCTATTAGTAGTACGATCGATCGATCGATCGATCGATCG 360
Db 301 TCGCTCTACAGTATGTCCTCTATTAGTAGTACGATCGATCGATCGATCGATCGATCG 360
QY 361 CGTTATAGAGCAGACAGACAGTGCATCTCGAATGTTTGGCTCAAAATGGTGGCTTTG 420
Db 361 TCTTATAGGGCTCAGACAGTGCATCTCGAATGTTTGGCTCAAAATGGTGGCTTTG 420
QY 421 ATACTGGCTTTCTTGGTCAATGCGCCCAATGATTTCTGGCTTCGGATTTCTTGGAGAAC 480
Db 421 ATACTGGCTTTCTTGGTCAATGCGCCCAATGATTTCTGGCTTCGGATTTCTTGGAGAAC 480
QY 481 ACCAACACAGAGAGTGGAGCGCTGCTTGTACGTAGTGATCGATCGATCGATCGATCG 540
Db 481 ACCAACACAGAGAGTGGAGCGCTGCTTGTACGTAGTGATCGATCGATCGATCGATCG 540
QY 541 GCATTCCTGGAAATTCCTGCTCCCTGCTCTCTGCTGCTCTATTTTCAAGTGTACAG 600
Db 541 ATGCTCTTGGAAATTCCTGCTCTCTGCTCTCTGCTGCTCTATTTTCAAGTGTACAG 600
QY 601 TGGAGCTCTGGAAGCGTGGAGTCTCAGTAGTGCTTGGCTAGCCACGCTGGATTCATCGCT 660
Db 601 TGGAGCTCTGGAAGCGTGGAGTCTCAGTAGTGCTTGGCTAGCCACGCTGGATTCATCGCT 660
QY 661 ACCTCTTCCAGGGGCACTGAGCACTCAGCAGAACTGGGTGGCTTGTAGGACAAGTCTTT 720
Db 661 ACCTCTTCCAGGGGCACTGAGCACTCAGCAGAACTGGGTGGCTTGTAGGACAAGTCTTT 720
QY 721 CTTGGATTAAGGAACCGCCGATCCCTTCAATTCAGAAAGTCCACGAGGAAAGAGCACT 780
Db 721 CTTGGATTAAGGAACCGCCGATCCCTTCAATTCAGAAAGTCCCTGAAAGAAAGAGAGC 780
QY 781 CTCTGCTGCTCTTAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAGTGGGTTC 840
Db 781 ATCTGCTGCTCTTAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAGTGGGTTC 840
QY 841 TTCTGCCGATCAGAAAGCCAGTGTCTTACCAGAGAGAGCAGTGGAGCTTCTCAGAGGC 900
Db 841 TTCTGCCGATCAGAAAGCCAGTGTCTTACCAGAGAGAGCAGTGGAGCTTCTCAGAGGC 900
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QY 901 AGGAAGCTAGCCAGGTGCTAGCTGCTCCTGAGTGTCTTTTGGCATTTTGGGCTCCG 960
Db 901 AGGAAGCTAGCCAGGTGCTAGCTGCTCCTGAGTGTCTTTTGGCATTTTGGGCTCCG 960
QY 961 TATTCGCTGTTTCAAAATTTGTTTCAACTTATCCGAGAGGGAGGCGCCCAATCGATT 1020
Db 961 TATTCGCTGTTTCAAAATTTGTTTCAACTTATCCGAGAGGGAGGCGCCCAATCGATT 1020
QY 1021 TGCTACAGCATAGCTTTTGGCTTACAGTGGTTTCAATTTCACTTATTATCCCTTTCTATAC 1080
Db 1021 TGCTACAGCATAGCTTTTGGCTTACAGTGGTTTCAATTTCACTTATTATCCCTTTCTATAC 1080
QY 1081 CCTTTGTGCCACAGACGTTTCCAGAGGCTTTCTGGAAGATCTCTGTGTGCAAGCA 1140
Db 1081 CCTTTGTGTCCAGAGGCTTTTCCAGAGGCTTTCTGGAAGATCTTTGTGTGCAAGCA 1140
QY 1141 CCAGACCTTTCACAGACCAGTCAGTATCTTCTTGA 1176
Db 1141 CCAGAGCTGTCCAGAACCAAGTCAGTATCTTCTTGA 1176

RESULT 5
US-10-626-126-5
; Sequence 5, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-126-5

Query Match      81.5%; Score 958.4; DB 9; Length 1176;
Best Local Similarity 88.4%; Pred. No. 6.4e-295;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 1 ATGTGGAGTCTAAGCGCACTGACGCTTGGCCACTGACTGCTCAAGTCCCTTGGCATTT 60
Db 1 ATGTGGAGTCTAAGCGCACTGACGCTTGGCCACTGACTGCTCAAGTCCCTTGGCATTT 60
QY 61 TTAATGTCCTGCTGCTCTTTTGGCTATACGATAGGCAATGCTGTGCTCAATTTAGCCTTT 120
Db 61 TTAATGTCCTGCTGCTCTTTTGGCTATACGATAGGCAATGCTGTGCTCAATTTAGCCTTT 120
QY 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCTT 180
Db 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCTT 180
QY 181 GACTTCTCTGTGGGTGTCATCTCCATCTCTGTATACATCCCTCACACGCTGTTAACTG 240
Db 181 GACTTCTCTGTGGGTGTCATCTCCATCTCTGTATACATCCCTCACACGCTGTTAACTG 240
QY 241 AATTTTGGAGTGGAAATCTGCATGTTTGGCTCATTAAGTACTATCTTTGTGCACAGCA 300
Db 241 AATTTTGGAGTGGAAATCTGCATGTTTGGCTCATTAAGTACTATCTTTGTGCACAGCA 300
QY 301 TCGCTCTACAGTATGTCCTCTATTAGTAGTACGATCGATCGATCGATCGATCGATCG 360
Db 301 TCGCTCTACAGTATGTCCTCTATTAGTAGTACGATCGATCGATCGATCGATCGATCG 360
QY 361 CGTTATAGAGCAGACAGACAGTGCATCTCGAATGTTTGGCTCAAAATGGTGGCTTTG 420
Db 361 TCTTATAGGGCTCAGACAGTGCATCTCGAATGTTTGGCTCAAAATGGTGGCTTTG 420
QY 421 ATACTGGCTTTCTTGGTCAATGCGCCCAATGATTTCTGGCTTCGGATTTCTTGGAGAAC 480
Db 421 ATACTGGCTTTCTTGGTCAATGCGCCCAATGATTTCTGGCTTCGGATTTCTTGGAGAAC 480
QY 481 ACCAACACAGAGAGTGGAGCGCTGCTTGTACGTAGTGATCGATCGATCGATCGATCG 540
Db 481 ACCAACACAGAGAGTGGAGCGCTGCTTGTACGTAGTGATCGATCGATCGATCGATCG 540
QY 541 GCATTCCTGGAAATTCCTGCTCCCTGCTCTCTGCTGCTCTATTTTCAAGTGTACAG 600
Db 541 ATGCTCTTGGAAATTCCTGCTCTCTGCTCTCTGCTGCTCTATTTTCAAGTGTACAG 600
QY 601 TGGAGCTCTGGAAGCGTGGAGTCTCAGTAGTGCTTGGCTAGCCACGCTGGATTCATCGCT 660
Db 601 TGGAGCTCTGGAAGCGTGGAGTCTCAGTAGTGCTTGGCTAGCCACGCTGGATTCATCGCT 660
QY 661 ACCTCTTCCAGGGGCACTGAGCACTCAGCAGAACTGGGTGGCTTGTAGGACAAGTCTTT 720
Db 661 ACCTCTTCCAGGGGCACTGAGCACTCAGCAGAACTGGGTGGCTTGTAGGACAAGTCTTT 720
QY 721 CTTGGATTAAGGAACCGCCGATCCCTTCAATTCAGAAAGTCCACGAGGAAAGAGCACT 780
Db 721 CTTGGATTAAGGAACCGCCGATCCCTTCAATTCAGAAAGTCCCTGAAAGAAAGAGAGC 780
QY 781 CTCTGCTGCTCTTAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAGTGGGTTC 840
Db 781 ATCTGCTGCTCTTAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAGTGGGTTC 840
QY 841 TTCTGCCGATCAGAAAGCCAGTGTCTTACCAGAGAGAGCAGTGGAGCTTCTCAGAGGC 900
Db 841 TTCTGCCGATCAGAAAGCCAGTGTCTTACCAGAGAGAGCAGTGGAGCTTCTCAGAGGC 900
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Db 361 TCCTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAATGGTGGCTGTTGG 420
Qy 421 ATACTGGCTTCTTGGTCAATAGGCCCAATGATTCTGGCTTCGGATTCCTTGGAAAGACAGC 480
Db 421 ATACTGGCTTCTTGGTCAATAGGCCCAATGATTCTGGCTTCAGATTCTTGGAAAGACAGC 480
Qy 481 ACCAAACACAGAGGAGTCGAGCCTGGCTTGTGTTACTAGTGGTACATCTCGCCATTAC 540
Db 481 ACGAACAAAGGACTGTGAGCCTGGCTTGTGTTACTAGTGGTACATCTCGCCATTAC 540
Qy 541 GCATTTCTGGAAATTCCTGCTCCCTGCTCTCTGTTGGTGTATTTCACTGTACAGATTAC 600
Db 541 ATGCTCTTGGAAATTCCTGCTCCCTGCTCATCTCTGGCTTATTTCAATGTACAGATTAC 600
Qy 601 TGGAGCCTGTGGAAGCCTGGAGTCTCAGTAGTGGCTTACGACCGCTGGATTCACTCGCT 660
Db 601 TGGAGCCTGTGGAAGCCTGGAGTCTCAGTAGTGGCTTACGACCGCTGGATTCACTCGCT 660
Qy 661 ACCTCTTCCAGGGCACTGACACTCAGCAGACTGGCTGGCTTGTAGGCAAGTCTT 720
Db 661 ACCTCTTCCAGTGTCTTACAGACACTTACACAGAGCTGGGTGGCTTGTAGGCAAGTAA 720
Qy 721 CCTGGATTAAGGAACACAGCGCATCCCTTCAATTCAGAAAGTCCACGAGGAAGAGCAGT 780
Db 721 CCTGGATTAAGGAACACAGCTGCATCTCGTCACTCAGAAAGTCTCGAAGAAAGAGCAGC 780
Qy 781 CTCTGTGTCTTAAAGACTCAATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
Db 781 ATCTGTGTCTTAAAGACTCAATGAGCACTCAATGAGCAAGTATCACTGCTTCAAAGTGGGTTC 840
Qy 841 TTCTGCCGATCAGAAAGCCAGTCTTCAACGAGAGAGCAGCTGGAGCTTCTCAGAGGC 900
Db 841 TTCTGCCGATCAGAAAGCTTCAGAGCTTTCGCAAGAGGAGTACCGAGAGCTTCTCAGAGGC 900
Qy 901 AGAAGCTAGCAGTCTGCTAGTGTCTCTCTGAGTCTTGTGCAATTTGCTGGCTCCG 960
Db 901 AGAAGCTAGCAGTCTGCTAGTGTCTCTCTGAGTCTTGTGCAATTTGCTGGCTCCG 960
Qy 961 TATTGCTGTTCACAAATGTTCTTCAACTTATCGCAGAGGGAGCGCCCAATCGATT 1020
Db 961 TACTGTCTGTTCACAAATGTTCTTCAACTTATCGCAGAGGGAGCGCCCAATCGATT 1020
Qy 1021 TGGTACAGATAGCCTTTGGCTACAGTGGTCAATTCATTTAATCCCTTCTATAC 1080
Db 1021 TGGTACAGATAGCCTTTGGCTACAGTGGTCAATTCATTTAATCCCTTCTATAC 1080
Qy 1081 CCTTTGTCACAGACCTTTCCAGAGCTTCTGGAAGATACCTCTGTGTGACAAAGCAA 1140
Db 1081 CCTTTGTCACAGACCTTTCCAGAGCTTCTGGAAGATACCTTTGTGTGACAAAGCAA 1140
Qy 1141 CCAGCAGCTTTCACAGACCCAGTCACTGATCTTCTTGA 1176
Db 1141 CCAGCAGCTTTCACAGACCCAGTCACTGATCTTCTTGA 1176
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RESULT 6

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US-10-626-398-5
; Sequence 5, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2
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; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-398-5
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Query Match 81.5%; Score 958.4; DB 9; Length 1176;

Best Local Similarity 88.4%; Pred. No. 6.4e-295;

Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

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Qy 1 ATGTGGAGTCTAAAGGCACTGACGCTCTTGCCACTGACTGCTCAAGTCCCTTGGCAATTT 60
Db 1 ATGTGGAGTCTAAAGGCACTGACGCTCTTGCCACTGACTGCTCAAGTCCCTTGGCAATTT 60
Qy 61 TTAATGTCCTGCTGCTTGTGCTAATACGATAGGCAATGCTGTGGTCATTTTAGCCCTTT 120
Db 61 TTAATGTCCTGCTGCTTGTGCTAATACGATAGGCAATGCTGTGGTCATTTTAGCCCTTT 120
Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAATTAATTTTCTTAATTTGGCTATTTCT 180
Db 121 GTAGCAGACAGAAACCTTAGACATCGAAATTAATTTTCTTAATTTGGCTATTTCT 180
Qy 181 GACTTCTTGTGGTGTCTCATCTTCTGTGATCCTCTCACGCTGTGTTAACTGG 240
Db 181 GACTTCTTGTGGTGTGATTTCCATTCCTCTGTATCCTCTCACGCTGTGTTAACTGG 240
Qy 241 AATTTTGGAGTGGATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGGCAGCA 300
Db 241 AATTTTGGAGTGGATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGGCAGCA 300
Qy 301 TCCGTCTACAGTATGTCTCTTACGATCGATACCACTGAGTCAGTTCATAAGCGCTGTG 360
Db 301 TCTGTCTACATATGTTCTCTCATTTAGCTAGATCGATACCACTGAGTTCATAAGCGCTGTG 360
Qy 361 CGTTATAGAGCAGACACACTGGCATCTCTGAAATTTGTTCTCAATGGTGGCTGTTGG 420
Db 361 TCTTATAGGCTCAACACACTGGCATCTCAAGATTTGTTCTCAATGGTGGCTGTTGG 420
Qy 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATTTGGCTTCGGATTCGGATTTGGAGAACAGC 480
Db 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATTTGGCTTCGGATTTGGAGAACAGC 480
Qy 481 ACCAAACACAGAGGAGTCGAGCCTGGCTTGTGTTACTAGTGGTACATCTCGCCATTAC 540
Db 481 ACCAAACACAGAGGAGTCGAGCCTGGCTTGTGTTACTAGTGGTACATCTCGCCATTAC 540
Qy 541 GCATTTCTGGAAATTCCTGCTCCCTGCTCTCTGTTGGTGTATTTCACTGTGACAGATTAC 600
Db 541 ATGCTCTTGGAAATTCCTGCTCCCTGCTCATCTCTGGCTTATTTCAATGTACAGATTAC 600
Qy 601 TGGAGCCTGTGGAAGCCTGGAGTCTCAGTAGTGGCTTACGACCGCTGGATTCACTCGCT 660
Db 601 TGGAGCCTGTGGAAGCCTGGAGTCTCAGTAGTGGCTTACGACCGCTGGATTCACTCGCT 660
Qy 661 ACCTCTTCCAGGGCACTGACACTCAGCAGACTGGCTGGCTTGTAGGCAAGTCTT 720
Db 661 ACCTCTTCCAGTGTCTTACAGACACTTACACAGAGCTGGGTGGCTTGTAGGCAAGTAA 720
Qy 721 CCTGGATTAAGGAACACAGCGCATCCCTTCAATTCAGAAAGTCCACGAGGAAGAGCAGT 780
Db 721 CCTGGATTAAGGAACACAGCTGCATCTCGTCACTCAGAAAGTCTCGAAGAAAGAGCAGC 780
Qy 781 CTCTGTGTCTTAAAGACTCAATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
Db 781 ATCTGTGTCTTAAAGACTCAATGAGCACTCAATGAGCAAGTATCACTGCTTCAAAGTGGGTTC 840
Qy 841 TTCTGCCGATCAGAAAGCCAGTCTTCAACGAGAGAGCAGCTGGAGCTTCTCAGAGGC 900
Db 841 TTCTGCCGATCAGAAAGCTTCAGAGCTTTCGCAAGAGGAGTACCGAGAGCTTCTCAGAGGC 900
Qy 901 AGAAGCTAGCAGTCTGCTAGTGTCTCTCTGAGTCTTGTGCAATTTGCTGGCTCCG 960
Db 901 AGAAGCTAGCAGTCTGCTAGTGTCTCTCTGAGTCTTGTGCAATTTGCTGGCTCCG 960
Qy 961 TATTGCTGTTCACAAATGTTCTTCAACTTATCGCAGAGGGAGCGCCCAATCGATT 1020
Db 961 TACTGTCTGTTCACAAATGTTCTTCAACTTATCGCAGAGGGAGCGCCCAATCGATT 1020
Qy 1021 TGGTACAGATAGCCTTTGGCTACAGTGGTCAATTCATTTAATCCCTTCTATAC 1080
Db 1021 TGGTACAGATAGCCTTTGGCTACAGTGGTCAATTCATTTAATCCCTTCTATAC 1080
Qy 1081 CCTTTGTCACAGACCTTTCCAGAGCTTCTGGAAGATACCTCTGTGTGACAAAGCAA 1140
Db 1081 CCTTTGTCACAGACCTTTCCAGAGCTTCTGGAAGATACCTTTGTGTGACAAAGCAA 1140
Qy 1141 CCAGCAGCTTTCACAGACCCAGTCACTGATCTTCTTGA 1176
Db 1141 CCAGCAGCTTTCACAGACCCAGTCACTGATCTTCTTGA 1176
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QY 961 TATTGCGTGTTCACAAATGTTCTTTCAACTTATCGCAGAGGGGAGCGCCCCAAATCGATT 1020
Db 961 TACTGTCTGTTCACAAATGTTCTTTCAACTTATCGCCAGAACGGAACGCCCCCAATCGGTG 1020
QY 1021 TGGTACAGCATAGAGCTTTTGGCTACAGTGGTTCAATTCATTATTAATCCCTTTCTATAC 1080
Db 1021 TGGTACAGCATAGAGCTTTTGGCTGCAATGGTTCAATTCGTTTGAATCCCTTTCTGTAC 1080
QY 1081 CCTTTGGCCACAGAGCTTTCCAGAGGCTTTCTGGAAGCTTCTGGAAGATATCTGTGTGACAAAGCAA 1140
Db 1081 CCTTTGGTCCAGAGGCTTTCCAGAGGCTTTCTGGAAGATATCTTTGTGTGACAAAGCAA 1140
QY 1141 CCAGCACCTTTCACAGACCCAGTCAGTATCTTCTTTGA 1176
Db 1141 CCAGGCGTGTTCACAGAACCAAGTCAGTATCTTCTTTGA 1176

RESULT 7
US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1

Query Match 56.9%; Score 669; DB 3; Length 1173;
Best Local Similarity 74.2%; Pred. No. 2.2e-202; Mismatches 295; Indels 9; Gaps 2;
Matches 875; Conservative 0;

QY 1 ATGTCGGAGTCTAACGGCACTGACGCTCTGCCACTGACTGCTCAAGTCCCTTGGCATTT 60
Db 1 ATGCCAGATACTAATAGCAACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
QY 61 TTAATGTCCTGCTGTTGTTTGTATTAACGATAGGCAATGCTGTGTCATTTTAGCCTTT 120
Db 61 TTTATGTCTCTTAGTAGCTTTTGTCTAATGCTAGGAAATGCTTTGGTCAATTTTAGCTTTT 120
QY 121 GTAGCAGACAGAAACCTTACACATCGAAGTAATATTTTTCCTAATTTGGCTATTCTT 180
Db 121 GTGGTGACAAAACCTTAGACATCGAAGTAGTATATTTTTCCTTAACCTTGGCCATCTCT 180
QY 181 GACTTCTTCGTGGGTGTCACTCCATTCCTCTGTACATCCCTCACAGCGCTTTTAACTGG 240
Db 181 GACTTCTTCGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCGTGTTCGAATGG 240
QY 241 AATTTTGGAAAGTGGAATCTGCAATGTTTGGCTCAATTAAGTCAATCTTTGTGCAAGCA 300
Db 241 GAATTTGGAAAGGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTATGTATACAGCA 300
QY 301 TCCGTCTACAGTATGTCCTCAATAGCTACGATCGATACAGTCAGTTCAGAAAGCTGTG 360
Db 301 TCTGTATATAACATTTGTCCTCATCAGCTATGATCGATACCTGTGCAAGTCTCAATAGCTGTG 360
QY 361 CGTTATAGACACAGCACACTGGCATCTCTGAAAATTTGTTGCTCAAAATGTTGGTGTGG 420
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Db 361 TCTTATAGAACTCAACATATCTGGGTCCTTGAAGATTGTTACTCTGAATGTGGCCGTTGG 420
QY 421 ATACTGGCTTTCTTGTGTCATATGATTCGGCTTCGGATTCCTTGGAGAACAGCAGC 480
Db 421 GTGCTGGCCCTTCTTAGTGAATGGCCAAATGATTCAGATTTTCAGAGTCTTTGGAGGA --- 476
QY 481 ACCAACACAGAGAGAGTGCAGGCTGGCTTTGTTGTTACTAGTGGTACATCTCGCCATTACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTCTTGCCATCACA 534
QY 541 GCATTTCTTGAATTCCTGTCTCCCTGTCTCTTGGTGGTCTATTTTCAAGTGTACAGATTAC 600
Db 535 TCATTTCTTGAATTCGTGATTCCTGATTCCTGATTCATTTAGTCGCTTATTTCAACATGAATAT 594
QY 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTGTGCTTAGCTAGCCCTAGCCACGCTCGATTCATCGCT 660
Db 595 TGGAGCTGTGGAAGCGTGTATCATCTCAGTGTGCTCAAGAGCCATCTCTGCACTGCTGCT 654
QY 661 ACCTCTTCCAGGGGCACTGGACACTCACGCAGAACTGGGTGCTGGCTTGTAGGCAAGTCTTT 720
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QY 721 CTTGGATTAAGAACACGCGGATCCCTTCAATTCAGAAAGTCCACAGAGAAAGACAGT 780
Db 715 TCTGCATCGACAGAGTTCTCTGCATCTTTTCAATTCAGAGAGACAGAGGAGAAAGTAGT 774
QY 781 CTCCTGCTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAAGTGGGTTC 840
Db 775 CTCATGTTTTCTCAAGAACCAAGATGAATGAATCAATTCATTTCTCAAAATGGGTTC 834
QY 841 TTTCTGCCATCAGAAAGCCAGTGTCTCACAGAGAGACAGTGGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATTTCTGTAGCTCTTCAACAAAGGGAACATGTTGAACCTGTAGAGCC 894
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QY 961 TATTGCTGTTCACAAATGTTCTTTCACACTTATCGCAGAGGGGAGCGCCCCAAATCGATT 1020
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QY 1081 CCTTTGTGCCACAGAGCTTTCCAGAAAGGCTTTCTGGAAGATATCTGTGTGACAAAGCAA 1140
Db 1075 CCATTTGTGTACAAAGCGCTTCAAAAGGCTTTCTTGAATAATATTTTGTATAAAAAAGCAA 1134
QY 1141 CCAGCACCTTC--ACAGACCCAGTCAGTATCTTCTTTGA 1176
Db 1135 CCTTACCATCAACACACAGTCGTCAGTATCTTCTTAA 1173

RESULT 8
US-09-910-411-1
; Sequence 1, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; FILE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
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; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-910-411-1

Query Match      56.9%; Score 669; DB 3; Length 1173;
Best Local Similarity 74.28; Pred. No. 2.2e-202; Mismatches 295; Indels 9; Gaps 2;
Matches 875; Conservative 0;

QY 1 ATGTCGGAGTCTAAACGCACTGACGCTCTGCGCACTGCTCAAGTCCCTTTGGCAATTT 60
DB 1 ATGCCAGATCTAATAGCAACAATCAATTTATCACTAAGCACTGCTGTTAGCAATTT 60
QY 61 TTAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 TTAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAAATTTTCTTAATTTGGCTATTCT 180
DB 121 GTGCTGACAAACCTTAGACATCGAAGTAGTATTATTTTCTTAATTTGGCTATTCT 180
QY 181 GACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 AATTTGGAAGTGAATCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
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QY 301 TCGCTCTACAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 TCTGTATATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 CGTTATAGACACAGCAGCAGTGGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
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QY 421 ATACTGCTTCTTGGTCAATGCGCCCAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 GTGCTGCTTCTTGGTCAATGCGCCCAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 476
QY 481 ACCAACACAGAGGAGTCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCCATCACA 534
QY 541 GCATTCCTGGAATTCCTGCTCCCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 535 TCATTCCTGGAATTCCTGCTCCCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 594
QY 601 TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGGTGCTCCTAGCCAGCTGCTGCTGCTGCTGCT 660
DB 595 TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGGTGCTCCTAGCCAGCTGCTGCTGCTGCTGCT 654
QY 661 ACCTTCTCCAGGGCACTGACACTCAGCAGAACTGGTGGTGGTGGTGGTGGTGGTGGTGGT 720
DB 655 GTCTCTTCCAACTCTGTGACACTCAATTCAGAGGTAGACTATCTTCAAGGAGATCTCTTT 714
QY 721 CCTGGAATTAAGGAACCAAGCGCATCTCTTCAATTCAGAAAGTCCACGAGGAAGAGCAGT 780
DB 715 TCTGCATCGACAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 774
QY 781 CTCTGCTGTCTTAAAGACTCAATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
DB 775 CTCAATGTTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTTC 834
QY 841 TTCTGCCGATCAGAAACCCAGCTGCTTCAACAGAGAGCAGCTGGAGCTTCTCAGAGGC 900
DB 841 TTCTGCCGATCAGAAACCCAGCTGCTTCAACAGAGAGCAGCTGGAGCTTCTCAGAGGC 900

835 TTCTCCCAATCAGATTCTGTAGCTCTTCCAAAGGGAACATGTTGAACCTGCTTAGAGCC 894
901 AGGAAGCTAGCCAGGTGCTAGCTGCTCTCTGAGTCTTTTGGCAATTTGCTGGCTCCG 960
895 AGGAGATTAGCCAAAGTCACTGGGCAATCTCTTAGGGGTTTTTGTGTTGCTGGCTCCA 954
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1135 CCTCTACCATCAACAACAGTCGGTCAGTATCTTCTTAA 1173

RESULT 9
US-09-875-076-13
; Sequence 13, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huang T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
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; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 60/157,293
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 60/157,282
 ; PRIOR FILING DATE: 1999-10-01
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 1173
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-875-076-13

Query Match 56.9%; Score 669; DB 3; Length 1173;
 Best Local Similarity 74.2%; Pred. No. 2.2e-202;
 Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

QY	1	ATGTCGGAGTCTAAGCGCACTGACGCTCTGCGCACTGCTCTCAAGTCCCTTGGCATTTT	60
DB	1	ATGCCAGATACTAATAGCAACAATTAATTTATCACTAAGCACTCGGTGTACTTTAGCATTT	60
QY	61	TTAATGTCCTGCTCTGCTTTTGTCTATAAGATAGGCAATGCTGTGGTCAATTTAGCCCTTT	120
DB	61	TTTAATGCTCTTAGTAGCTTTTGCTATTAATGCTAGGAATGCTTTGGTCAATTTTAGCTTTT	120
QY	121	GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTTTTCTTAATTTGGCTATTCT	180
DB	121	GTGGTGGACAAAAACCTTAGACATCGAAGTAGTATTTTTTTCTTAATTTGGCCATCTCT	180
QY	181	GACTTCTTGGTGGTGTATCTCCATCTCTGTATCATCCCTCAACGCTGTTAACTGG	240
DB	181	GACTTCTTGGTGGTGTATCTCCATCTCTGTATCATCCCTCAACGCTGTTGGAATGG	240
QY	241	AATTTTGGAGTGGAAATCGCATGTTTGGCTCATCTACTGACTATCTTTTGGCAGCA	300
DB	241	GATTTTGGAAAGGAAATCTGTATTTTGGCTCAGTACTGACTATCTTTTATGACAGCA	300
QY	301	TCCGCTCTACAGTATTGCTCTCATTAGCTACGATACGATCCAGTTCAGTTTCAACGCTGTG	360
DB	301	TCGTATATAACATTTGCTCTCATCAGTATGATCATCTGTCAGTCTCAATGCTGTG	360
QY	361	CGTTATAGACACAGACACTGGCATCTCGAAATATGTTGTCTAAAGTGGCTGTTTGG	420
DB	361	TCATTATAGAACTCAACATACTGGGGTCTTGAAGATGTTTACTCTGATGGTGGCGGTTGG	420
QY	421	ATACTGGCTTCTTGTGTCAATGGCCCAATGATCTTGGCTTCGGATTCCTTGAAGACAGC	480
DB	421	GTGCTGGCTTCTTAGTGAATGGCCCAATGATCTTGTAGTTTCAGAGTCTTGGAAAGA	476
QY	481	ACCAACACAGAGAGTGGAGGCTGTGCTTTGTTTACTGTAGTGTATCTCTCGCCATTAACA	540
DB	477	--TGAAGTAGTGAATGTGAACCTGGAATTTTTTTCGGAATGGTATCTCTTGGCATACA	534
QY	541	GCAATCTTGGAAATTCCTGCTCCCTGTCTCTCTGGTGGTCTATTTTCAGTGTACAGATTAC	600
DB	535	TCATTCTTGAATTTGTTGATCCAGTCATCTTAGTCGCTTATTTTCAACATGAATATTAT	594
QY	601	TGAGGCTGTGGAGCGTGGAGTCTCAGTAGGTGCCCTAGCCAGCTGGATTATCGCT	660
DB	595	TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGCCAAAGCCATCTCTGGACTGCT	654
QY	661	ACCTCTTCCAGGGGCACTGGACACTCACGACAACTGGGTGGCTTGTAGCACAGTCTT	720
DB	655	GTCTCTTCCAACATCTGTGGACACTCATTTTCAGAGGTAGACTATCTTCAAGGAGATCTCTT	714
QY	721	CCTGGATTAAAGAAACGACCGCATCCCTTCAATTCAGAAAGTCCACGAGGAAAGAGCAGT	780
DB	715	TCGTGATCGACAGAAGTCTCTGATCTCTTCAATTCAGAGACACAGAGGAGAGTAGT	774
QY	781	CTCCTGGTGTCTTAAGGACTCAATAGAGCGGTAGTATCATCGCTTCAAAAGTGGGTTC	840
DB	775	CTCATGTTTTCTTCAAGAACCAAGATGAATAGCAATACAATTTGCTTCCAAATAGGTTC	834

535 TCATTCTTGGAAATTCGTGATGCCAGTCATCTTAGTCGCTTATTTTCAACATGAATATTTAT 594
601 TGGAGCCTGTGGAAAGCGTGGAGTCTCAGTAGGTGGCCCTAGCCACGCTGGATTCATCGCT 660
595 TGGAGCCTGTGGAAAGCGTGGAGTCTCAGTAGGTGGCCACCAAGCCATCCTGGACTGACTGCT 654
661 ACCTCTTCCAGGGGCACTGGACACTCAGCAGAACTGGGTTGGCTTGTAGGACAAGTCTT 720
655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAGGAGATCTCTT 714
721 CTGGATTAAAGGAACAGCGCATCCCTCTTCAATTCAGAAAGTCCACGAGGAAGAGCAGT 780
715 TCTGCATCGACAGAAGTTCTGTGATCTCTTCAATTCAGAGAGCGAGGAGAGAGTAGT 774
781 CTCTGTGTCTTAAAGACTCAGTAGGCGGTAGTATCATCGCTTCAAAAGTGGGTCC 840
775 CTCTGTGTCTTAAAGACTCAGTAGGCGGTAGTATCATCGCTTCAAAAGTGGGTCC 834
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835 TTCTCCCAATCAGATCTGTAGCTCTTCCAAAGGGAACATGTTGAATGCTTAGAGCC 894
901 AGGAAGCTAGCCAGGTGGCTGTCTCTCAGTGTCTTTTGGCATTGCTGGGCTCCG 960
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961 TATTGCTGTTCACAAATGTTCTTCAACTTATCGCAGAGGGGAGCGCCCAATCGATT 1020
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1081 CCTTTTGGCCACAGACCTTTCCAGAGGCTTTCTGGAAGATPACTCTGTGCAAAAGCAA 1140
1075 CCATTGTGTCAAGCGCTTTCAAAGGCTTCTTGAANAATTTTGTATTAAGAAAGCAA 1134
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1135 CCTCTACCATCACAACACAGTCGGTCAGTATCTTCTTAA 1173

RESULT 13

US-10-272-983-13
; Sequence 13, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439

; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-983-13

Query Match 56.9%; Score 669; DB 6; Length 1173;

Best Local Similarity 74.2%; Pred. No. 2.2e-202; Indels 9; Gaps 2;
Matches 875; Conservative 0; Mismatches 295;

Qy 1 ATGTCGGAGTCTAAACGCACTGACGCTCTGCCCACCTGCTCAAGTCCCCTTGGCAATTT 60
Db 1 ATGCCAGATATAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60
Qy 61 TTAATGTCCTGCTGCTTTGCTTAACGATAGGCAATGCTGTGGTCATTTTACGCTTTT 120
Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCATTTTACGCTTT 120
Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180
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Db 181 GACTCTTCTGCTGGGTGTCTCCTCCTCCTTGTGTACATCCCTCACAAGCTGTTTAACTGG 240
Qy 241 AATTTGGAGTGGATCTGCATGTTTGGCTCATTAAGTACTATCTTTTGTGACAGCA 300
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Db 361 TCTTATAGAACTCAACATACTGGGCTTGAAGATTTGTTACTCTGATGGTGGCGTTGG 420
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Qy 481 ACCAACACAGAGGAGTGGAGCTGGCTTGTACTGAGTGGTACATCTCGCCATTTACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCCATCACA 534
Qy 541 GCATTTCTGGAAATTCCTGCTCCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
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Qy 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTACAGCCAGCTGGAATTCATCGCT 660
Db 595 TGGAGCTGTGGAAGCGTGGATCATCTCAGTAGGTGTCGCAAGCCATCTCTGCACTGCTGCT 654
Qy 661 ACCTCTTCCAGGGGCACTGGACACTCAGCAGAACTGGGTTGGCTTGTAGGACAAGTCTT 720
Db 655 GTCTCTTCCAAACATCTGTGGACACTCAATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 721 CCTGGATTAAAGGAACCAAGCCAGTCCCTTCAATTCAGAAAGTCCACGAGGAAGAGCAGT 780
Db 715 TCTGCATCGACAGAGTTCCTGATCTTCTGATCTTCAATTCAGAGAGACAGAGAGAGTAGT 774
Qy 781 CTCTGTGTCTTAAAGACTCAGTAGGCGGTAGTATCATCGCTTCAAAAGTGGGTCC 840
Db 775 CTCTGTGTCTTCAAGAACCAAGATGAATAGCAATCAATTTGCTTCCAAATGGGTCC 834
Qy 841 TTCTGCCGATCAGAAAGCCAGTCTTCCAGAGAGAGCAGTGGAGCTTCTCAGAGGC 900

Query Match	56.9%	Score 669	DB 6	Length 1173
Best Local Similarity	74.2%	Pred. No. 2.2e-202		
Matches 875	Conservative 0	Mismatches 295	Indels	Gaps 2
QY	1	ATGTCGAGGCTAAACGGCAGCTGAGTCTTGCCACCTGAGCTGCTCAAGTCCCTCGGCATTT	60	
DB	1	ATGCCAGATACTAATAGCACCAATCAATTTATCACTAAGCACTCGTGTTACTTTAGCATTT	60	
QY	61	TTAATGTCCCTGCTGCTTTTGGCTATTAACGATAGGCAATGCTGTGTCATTTTAAAGCCTTT	120	
DB	61	TTTATGTCTCTAGTAGCTTTTGGCTATAATGCTAGGAAATGCTTTGGTCAATTTAGCTTTT	120	
QY	121	GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTTTCTTAATTTGGCTATTCT	180	
DB	121	GTGCTGCACAAAACCTTAGACATCGAAGTAGTTATTTATTTTTTCTTAACCTTGGCCATCTCT	180	
QY	181	GACTTCTTGTGGGTGTGTCATCTCCATTCCTGTACATCCCTCACAGCTGCTTTAACTGG	240	
DB	181	GACTTCTTGTGGGTGTGAATCTCATTTCTTTTGTACATCCCTCACAGCTGTTTGGATGG	240	
QY	241	AAATTTTGGAAATGGAATCTGCATGTTTGGCTCAATTAAGTACTATCTTTTGTGCACAGCA	300	
DB	241	GAATTTTGGAAAGGAATCTGTGTAATTTGGCTCACTACTGACTATCTGTTATGTACAGCA	300	
QY	301	TCGGTCTACAGTATGTGCTCTCAATTAGCTACGATCGATACCAAGTCAGTTTCAAAACGCTGTG	360	
DB	301	TCTGTATATAACATGTCTCTCATCAGCTATGATCGATACCTGTGTCAGTCTCAAATGCTGTG	360	
QY	361	CGTTATAGACACAGCACACCTGGCATCTCGAAATTTGTGCTCAAAATGGTGGCTGTTTGG	420	
DB	361	TCCTTATAGAATCTCAACATACCTGGGGTCTTTGAAGATTTGTTACTGTATGGTGGCCGTTTGG	420	
QY	421	ATACTGGCTTTCTTGGTCAATGGCCCCAATGAATCTGGCTTCGGATTTCTTGAAGAACAGC	480	
DB	421	GTGCTGGCCTTCTTAGTGAATGGGCCAATGAATCTAGTTTCAGAGTCTTTGAAGGA	475	
QY	481	ACCAACACAGAGGAGTGGAGCCTGGCTTTGTTATCTGAGTGGTATCATCCTCGCCATTACA	540	
DB	477	--TGAAGGTAGTGAATGTGAACCTGGATTTTCTTTTGGAAATGGTATCATCTCTGGCCATCACA	534	

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Post-processing: Minimum Match 0%

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Database : Published Applications NA_NUS*

- 1: /SIDSS5/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 2: /SIDSS5/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /SIDSS5/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /SIDSS5/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /SIDSS5/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 6: /SIDSS5/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 7: /SIDSS5/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 8: /SIDSS5/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 9: /SIDSS5/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 10: /SIDSS5/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 11: /SIDSS5/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 12: /SIDSS5/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 13: /SIDSS5/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 14: /SIDSS5/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 15: /SIDSS5/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	268.4	22.8	1326	14	US-11-241-956-19 Sequence 19, Appl
2	138	11.7	2761	11	US-11-036-196-2003 Sequence 2003, Ap
3	138	11.7	2761	11	US-11-136-527-3990 Sequence 3990, Ap
4	133.6	11.4	2824	14	US-11-136-527-127 Sequence 127, App
5	79.8	6.8	2483	14	US-11-136-527-2847 Sequence 2847, Ap
6	74	6.3	1401	14	US-11-127-877-4 Sequence 4, Appli
7	66.6	5.7	2348	14	US-11-136-527-3691 Sequence 3691, Ap
8	66.6	5.7	3578	14	US-11-036-196-1495 Sequence 1495, Ap
9	66.6	5.7	4095	14	US-11-136-527-2030 Sequence 2030, Ap
10	66.4	5.6	2633	14	US-11-136-527-3114 Sequence 3114, Ap
11	60.6	5.2	2733	14	US-11-136-527-2435 Sequence 2435, Ap
12	59.6	5.1	2699	14	US-11-127-877-5 Sequence 5, Appli
13	56.4	4.8	1773	14	US-11-127-877-17 Sequence 17, Appl
14	56.4	4.8	1974	14	US-11-124-368A-14 Sequence 14, Appl
15	54.8	4.7	600	14	US-11-136-527-7845 Sequence 7845, Ap
16	54.8	4.7	1269	14	US-11-136-527-3749 Sequence 3749, Ap
17	54.2	4.6	2146	8	US-10-750-185-35936 Sequence 35936, A
18	54.2	4.6	2146	8	US-10-750-623-35936 Sequence 35936, A

19	51.2	4.4	3741	14	US-11-136-527-751	Sequence 751, App
20	50.2	4.3	1400	14	US-11-136-527-4223	Sequence 4223, Ap
21	50.2	4.3	1400	14	US-11-136-527-8086	Sequence 8086, Ap
22	47.6	4.0	1020	14	US-11-127-877-12	Sequence 12, Appl
23	47.6	4.0	1020	14	US-11-174-816-2	Sequence 2, Appli
24	47.6	4.0	1038	11	US-11-217-710-5	Sequence 5, Appli
25	46.2	3.9	1496	14	US-11-136-527-2608	Sequence 2608, Ap
26	46	3.9	1020	14	US-11-174-751-2	Sequence 2, Appli
27	43.8	3.7	1303	14	US-11-128-061-570	Sequence 570, App
28	43.8	3.7	1303	14	US-11-128-049-570	Sequence 46, Appl
C 29	43.6	3.7	85980	11	US-11-114-798-47	Sequence 47, Appl
C 30	43.6	3.7	197241	11	US-11-114-798-47	Sequence 3427, Ap
C 31	42.6	3.6	6501	14	US-11-136-527-3427	Sequence 3427, Ap
C 32	42.4	3.6	706	8	US-10-750-185-32790	Sequence 32790, A
C 33	42.4	3.6	706	8	US-10-750-623-32790	Sequence 32790, A
C 34	42.4	3.6	1928	14	US-11-136-527-3095	Sequence 3095, Ap
35	42.4	3.6	2509	14	US-11-136-527-3738	Sequence 3738, Ap
36	42	3.6	1055	14	US-11-174-751-4	Sequence 4, Appli
37	42	3.6	1056	14	US-11-174-816-4	Sequence 4, Appli
38	42	3.6	1056	14	US-11-174-751-5	Sequence 5, Appli
39	41.8	3.6	2591	14	US-11-136-527-1944	Sequence 1944, Ap
40	41	3.5	2809	14	US-11-136-527-2036	Sequence 2036, Ap
41	40.6	3.5	1116	14	US-11-216-610-5	Sequence 5, Appli
42	40.6	3.5	1193	14	US-11-216-610-3	Sequence 3, Appli
43	40.6	3.5	1689	14	US-11-216-610-1	Sequence 1, Appli
44	40.6	3.5	1915	14	US-11-068-686-3	Sequence 3, Appli
45	40.6	3.5	1945	14	US-11-127-877-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1

- US-11-241-956-19
- Sequence 19, Application US/11241956
- Publication No. US20060024792A1
- GENERAL INFORMATION:
- APPLICANT: INCYTE GENOMICS INC.; BAUGHN, Mariah R.;
- APPLICANT: GAUL Richard C.; CHAWLA, Narinder K.;
- APPLICANT: GANDHI, Ameena R.; HAFALIA, April J.A.;
- APPLICANT: RAMKUMAR, Jayalaxmi; TRIBOULEY, Catherine M.;
- APPLICANT: THORNTON, Michael B.; KALLICK, Deborah A.;
- APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;
- APPLICANT: BURFORD, Neil; KHAN, Farrah A.;
- APPLICANT: YUE, Henry; LU, Yan;
- APPLICANT: ARVIZU, Chandra S.; ROOPA, Reddy M.;
- APPLICANT: NGUYEN, Daniel B.; LEE, Ernestine A.;
- APPLICANT: LU, Dyung Alina M.; ISON, Craig H.;
- APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.
- TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
- FILE REFERENCE: PI-0236 USN
- CURRENT APPLICATION NUMBER: US/11/241,956
- CURRENT FILING DATE: 2005-10-04
- PRIOR APPLICATION NUMBER: US/10/398,036
- PRIOR FILING DATE: 2003-03-28
- PRIOR APPLICATION NUMBER: PCT/US01/30661
- PRIOR FILING DATE: 2001-09-28
- PRIOR APPLICATION NUMBER: US 60/245,855
- PRIOR FILING DATE: 2000-11-03
- PRIOR APPLICATION NUMBER: US 60/242,322
- PRIOR FILING DATE: 2000-10-20
- PRIOR APPLICATION NUMBER: US 60/240,589
- PRIOR FILING DATE: 2000-10-13
- PRIOR APPLICATION NUMBER: US 60/249,343
- PRIOR FILING DATE: 2000-11-15
- PRIOR APPLICATION NUMBER: US 60/247,587
- PRIOR FILING DATE: 2000-11-09
- PRIOR APPLICATION NUMBER: US 60/245,900
- PRIOR FILING DATE: 2000-11-03
- PRIOR APPLICATION NUMBER: US 60/242,223
- PRIOR FILING DATE: 2000-10-20
- PRIOR APPLICATION NUMBER: US 60/236,546
- PRIOR FILING DATE: 2000-09-29

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; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7474823CB1
US-11-241-956-19

Query Match      22.8%; Score 268.4; DB 14; Length 1326;
Best Local Similarity 77.8%; Pred. No. 7.8e-67;
Matches 339; Conservative 0; Mismatches 91; Indels 6; Gaps 1;

QY 194 GTGTGATCCATCTCTGTATACATCCCTCACAGCTGTTTAACTGGAATTTGGAGTG 533
Db 353 GTGTGATCCATCTCTGTATACATCCCTCACAGCTGTTTAACTGGAATTTGGAGTG 412
QY 254 GAATCTGCATGTTTGGCTCATTACTGACTATCTTTTGTGCACAGCATCGCTACAGTA 313
Db 413 AATCTGTGTATTTTGGCTCATTACTGACTATCTTTTGTGCACAGCATCTGTATATACA 472
QY 314 TTGTCTCTCAATAGCTACGATCGATACCAAGTCTAGTCTTCAAACGCTGTGCGTTATAGAGCAC 373
Db 473 TTGTCTCTCAATAGCTACGATCGATACCAAGTCTAGTCTTCAAACGCTGTGCGTTATAGAGCAC 532
QY 374 AGCAGACTGGCATCTCTGAAATTTGTCTCAATGTGTGGCTGTTTGGATACTGGCTTTCT 433
Db 533 AACATACTGGGGCTTTGAAAGATTTTACTCTGTATGTGTGGCGCTTGGGCTGCTGCTTCT 592
QY 434 TGGTCAATGSCCAATGATTTCTGGCTTCGGATTTCTGGATTTCTTGGAGAACACAGCAGAGG 493
Db 593 TAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAGGA-----TGAAGGTAGTG 646
QY 494 AGTGCAGGCTGGCTTTTGTGTACTGAGTGGTATACCTCGCCATTAACAGCATCTCTGGAAT 553
Db 647 AATGTGAACCTGGATTTTTCGGATTTGTTGGATTTGTTGGATTTGTTGGATTTCTGGAAT 706
QY 554 TCGTCTCCCTGTCTCTGTTGGTGGTCTATTTTCACTGATACAGATTTTACTGGAGCTCTGGA 613
Db 707 TCGTATCCAGTCATCTTAGTCTGCTTATTTTCAACATGAATATTTATTGGAGCTCTGGA 766
QY 614 AGCGTGGAGTCTCAG 629
Db 767 AGCGTGAATCACTCAG 782
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RESULT 2

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US-11-036-196-2003
; Sequence 2003, Application US/11036196
; Publication No. US20060078900A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/11/036,196
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US/10/152,319
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
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; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2003
; LENGTH: 2761
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_053506
US-11-036-196-2003
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Query Match 11.7%; Score 138; DB 11; Length 2761;

Best Local Similarity 55.0%; Pred. No. 5.7e-29;

Matches 317; Conservative 0; Mismatches 250; Indels 9; Gaps 2;

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QY 51 CTTGGCAATTTTAAATGTCCTCTGCTTTTGTCTATACGATAGGCAATGCTGTGTGCAT 110
Db 445 CTTGGCTGGCTCCTGCTGCTCATCTGCGCCACAGTACTGGGCAACGCGTGTGCAT 504
QY 111 TTTAGCCTTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAAATTT 170
Db 505 GCTGCGCTTCGTGGCGGATTCGAGCCTCGGACCCAGAAACAACTCTTCTGTCAACCT 564
QY 171 GGCATTTTCTGACTTCTGCTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACAGCT 230
Db 565 CGCCATCTCCGACTTCTCTGCTGGGTGCTTCTGTCATCCCATTTGTACGTACCTTATGTGCT 624
QY 231 GTTTAAAC---TGGAAATTTTGGAAATCTGCAATGTTTGGCTCATTTACTGACTATCT 287
Db 625 GACCGGCGCTTGGACCTTTCGCGGGGCTCTGCAAGCTGTGGCTGGTGTAGACTACCT 684
QY 288 TTTGTGCACAGCATCCGCTCTACAGTATTTCTCTCATTTAGTACGATCGATACAGTCACT 347
Db 685 ACTGTGTGCTCTCTCGTCTTCAACATCGTACTCTCATCGATATGACCGGATTCCTGTCACT 744
QY 348 TTCAAACGCTGTGCGTTATAGAGCACAGCACACTGSCATCTCGAAATTTGTTGCTCAAAAT 407
Db 745 CACTCGAGCTGTCTCTACAGGGCCCGACGAGGGGGGACACAGACGGGCGCTTCGGAAGAT 804
QY 408 GGTGGCTGTTTGGATACTGGCTTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGAT-- 465
Db 805 GGCACTGGTGTGGGTGCTGGCTTCTCTGTGTATGGGCTGCGCATCTCGATTGGGAGTA 864
QY 466 ----TCTTGGAAAGAACAGACCAACACAGAGAGTGGAGCCCTGGCTTGTGTACTGAGTG 521
Db 865 CTTGCTGGTGGCAGTTTCCATCCCGAGGGCCACTGCTATGTGTAGTCTTCTTACAACTG 924
QY 522 GTACATCTTCGCCATTTACAGCATTTCTTGAATTTCTGCTCCCTGTCTCTTGTGTGCTA 581
Db 925 GTACTTTTTCATCAGCGGCTTCCACCTCGAGTTCTTACGCGCTTCTCAGCGCTTACCTT 984
QY 582 TTTTCAGTGTACAGATTTTACTTGGAGCCTGTGGAGCG 617
Db 985 CTTCAACCTCAGCATCTACTCTGACATCCAGAGCG 1020
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RESULT 3

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US-11-136-527-3990
; Sequence 3990, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
```


; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3990
; LENGTH: 2814
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3990

Query Match 11.7%; Score 138; DB 14; Length 2814;
Best Local Similarity 55.0%; Pred. No. 5.7e-29;
Matches 317; Conservative 0; Mismatches 250; Indels 9; Gaps 2;

QY 51 CTTGGCATTTTTAATGTCCTGCTGCTTTTGTCTATACGATAGGCAATGCTGGTGCAT 110
DB 435 CTTGGCTGGCTCATGGGCTGCTCATCGTGGCCACAGTACTGGGCAACGGCTGGTGCAT 494

QY 111 TTAGGCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTT 170
DB 495 GCTGGCTTGTGGGCGATTCGAGCCTCCGACCCAGACAACTTCTTCTGCTCAACCT 554

QY 171 GGCTATTCTGACTTCTTGGGGTGTGATCTCCATCTCTGTATACATCCCTCACAGCT 230
DB 555 CGCCATCTCGACATCTCTCGGGTGTGCTTCTGATCCCATGTTGATGCTATGCT 614

QY 231 GTTTAAAC---TGGAAATTTGGAGTGAATCTGATGTTGGTCAATTAAGTACTATCT 287
DB 615 GACCGGCGTTGGACCTTCGGCGGGGCGCTTGCAGCTGTGGTGTGGTAGACTACCT 674

QY 288 TTGTGACAGCATCCGCTTACAGTATTGTCTCATTTAGCTACGATACGATACCACTCAGT 347
DB 675 ACTGTGCGCTCTCTCGCTTCAACATCGTACTCATAGTATGACCGATTCCTGTGCTCAGT 734

QY 348 TTCAAACGCTGTGGTGTATAGACACAGCAACATCGGCATCTGAAATTTGTGCTCAAT 407
DB 735 CACTCGAGCTGTCTCTACAGGGGCCAGAGGGGGACACAGAGCGGGCGTTCGGAAGAT 794

QY 408 GGTGGCTGTTGGATCTGCTTCTTGGTCAATGGGCCCAATGATTTGCGCTTCGGAT-- 465
DB 795 GGCACTGGTGTGGTGTGGCTTCTGCTGTATGGGCTTGCCTATCTGAGTTGGGAGTA 854

QY 466 ----TCTTGAAGAACAACAGCAACACAGAGGAGTGGAGCTTGTGTTACTGAGTG 521
DB 855 CTTGCTGTGGGCGAGTTCATCCCGAGGGCCACTGCTATGCTGAGTCTTCTACAACTG 914

QY 522 GTACATCTCGCCATTAACAGCATTTTGGAAATTCCTGCTCCCTGCTCTCTGTTGGTGTCTA 581
DB 915 GTACTTTCTCATCGGCTCCACCTCGAGTCTTTCAGCGCTTCTCCTCAGCGTTACCTT 974

QY 582 TTTCAAGTGTACAGATTTACTGGAGCGCTGTGGAAGCG 617
DB 975 CTTCAACCTCAGCATCTACCTGAACATCCAGAGCG 1010

RESULT 4
US-11-136-527-127
; Sequence 127, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127
; LENGTH: 2824
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-127

Query Match 11.4%; Score 133.6; DB 14; Length 2824;
Best Local Similarity 52.1%; Pred. No. 1.1e-27;
Matches 300; Conservative 19; Mismatches 248; Indels 9; Gaps 2;

QY 51 CTTGGCATTTTTAATGTCCTGCTGCTTTTGTCTATACGATAGGCAATGCTGGTGCAT 110
DB 445 CTTGGCTGGCTCATGGGCTGCTCATCGTGGCCACAGTACTGGCAACGGCTGGTGCAT 504

QY 111 TTAGGCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTT 170
DB 505 GCTCGCTTGTGGGCGATTCGAGCCTCCGACCCGSRGCMACRWCYTMKTKYKWCMAASCT 564

QY 171 GGCTATTCTGACTTCTTGGGGTGTGATCTCCATCTCTGTATACATCCCTCACAGCT 230
DB 565 YRSAAKCTCSGAKWKSSTCGTGGTGCCTTCTGATCCCCATTTGATACCTATGTGCT 624

QY 231 GTTTAAAC---TGGAAATTTGGAAAGTGAATCTGATGTTGGTCAATTAAGTACTATCT 287
DB 625 GACCGGCGTTGGACCTTCGGCGGGGCGCTTGCAGCTGTGGTGTGGTAGACTACCT 684

QY 288 TTGTGACAGCATCCGCTTACAGTATTGTCTCATTTAGCTACGATACGATACCACTCAGT 347
DB 685 ACTGTGCGCTCTCTCGCTTCAACATCGTACTCATCAGCTATGACCGATTCCTGTGCTCAGT 744

QY 348 TTCAAACGCTGTGGTGTATAGACACAGCAACATCGGCATCTGAAATTTGTGCTCAAT 407
DB 745 CACTCGAGCTGTCTCTACAGGGGCCAGAGGGGGACACAGAGCGGGCGTTCGGAAGAT 804

QY 408 GGTGGCTGTTGGATCTGCTTCTTGGTCAATGGGCCCAATGATTTGCGCTTCGGAT-- 465
DB 805 GGCACTGGTGTGGTGTGGCTTCTGCTGTATGGGCTTGCCTATCTGAGTTGGGAGTA 864

QY 466 ----TCTTGAAGAACAACAGCAACACAGAGGAGTGGAGCTTGTGTTACTGAGTG 521
DB 865 CTTGCTGTGGGCGAGTTCATCCCGAGGGCCACTGCTATGCTGAGTCTTCTACAACTG 924

QY 522 GTACATCTCGCCATTAACAGCATTTTGGAAATTCCTGCTCCCTGCTCTCTGTTGGTGTCTA 581
DB 925 GTACTTTCTCATCGGCTCCACCTCGAGTCTTTCAGCGCTTCTCCTCAGCGTTACCTT 984

QY 582 TTTCAAGTGTACAGATTTACTGGAGCGCTGTGGAAGCG 617
DB 985 CTTCAACCTCAGCATCTACCTGAACATCCAGAGCG 1020

RESULT 5
US-11-136-527-2847
; Sequence 2847, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2847
; LENGTH: 2483
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2847

Query Match 6.8%; Score 79.8; DB 14; Length 2483;
Best Local Similarity 55.3%; Pred. No. 3.7e-12;
Matches 172; Conservative 2; Mismatches 134; Indels 3; Gaps 1;

QY 73 CTTGCTTTTGTCTAATAGGATAGGCAATGCTGTGCTCATTTTATAGCCCTTTGTAGCAGACAGA 132
DB 548 CTCAGTCTGTGTGACCATCATTTGGGAACATTTCTGGTCATGTTTCCATTAAAGTCARCCGC 607

QY 133 AACCTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTTCTGACTTCTTCGTG 192
DB 608 CACCTTCAGACTGTCAACAATTTACTTCTGTTGAGCTGGCCCTGTGCTGACCTCATCAT 667

QY 193 GGTGTCTCATCTCCATTCCTCTGTATACCTCCCTCACAGCTGTTT---AACTGGAAATTTTGA 249
DB 668 GGTGTTTCTCCATGAACCTGTATACCTCTACACTGTGATTGGCTACTGGCCCTTTGGGA 727

QY 250 AGTGGAAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGACAGCATCCGCTCTAC 309
DB 728 CCTGTAGTATGTGACCTTGTGGCTAGCATTTGGCACTATGTTGTACAGCAATGCTCCCGTTATG 787

QY 310 AGTATTCTCTCATTAAGTACGATCGATACCACTGCTTCAAACTGCTGCGTTATAGA 369
DB 788 AATCTCTCATCATCAGCTTGTATAGATCTTCTGTGTACGAAACCTCTGACCTACCCA 847

QY 370 GCACAGCACAC 380
DB 848 GTTAAGCGGAC 858

RESULT 6
US-11-127-877-4
; Sequence 4, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-4

Query Match 6.3%; Score 74; DB 14; Length 1401;
Best Local Similarity 53.1%; Pred. No. 1.3e-10;
Matches 205; Conservative 0; Mismatches 175; Indels 6; Gaps 2;

QY 73 CTTGCTTTTGTCTAATAGGATAGGCAATGCTGTGCTCATTTTATAGCCCTTTGTAGCAGACAGA 132
DB 97 CTCAGTTTGTGTGACCATTTATTCGGGAACATCTTAGTCATGTTTCCATTAAAGTCARCCGC 156

QY 133 AACCTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTTCTGACTTCTTCGTG 192
DB 157 CACCTCCAGACCGCTCAACAATTTACTTTTATTACGCTTGGCCCTGTGCTGACCTTATCAT 216

QY 193 GGTGTCTCATCTCCATTCCTCTGTATACCTCCCTCACAGCTGTT---TAACTGGAAATTTTGA 249
DB 217 GGTGTTTCTCCATGAACCTTGTACCCCTCTACACTGTGATTGGTTACTGGCCCTTTGGGA 276

QY 250 AGTGGAAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGACAGCATCCGCTCTAC 309

DB 277 CCTGTGGTGTGACATCGCTTTGGCTAGCCCTGGACTATGTGGTCAGCAATGCCCTCAGTTATG 336
QY 310 AGTATTGTCTCTCATTTAGCTACCATCGATACCACTAGTTTCAAACTGCTGTGCGTTATAGA 369
DB 337 AATCTGCTCATCATCATCTTTGACAGGTACTTCTGTGTCAAAAACCTCTGACCTTACCCA 396
QY 370 GCACAGCACATCGGCAATCTGAAATTTGTTGCTCAAAATGGTGGCTGTTTGGATACTGGCT 429
DB 397 GTCAGGCGGACCAAAAATGGCA---GGTATGATGATTGTCAGCTGCCTGGGTCTCTCT 453

QY 430 TTTCTTGGTCAATGGGCCCAATGATTCT 455
DB 454 TTTATCTCTCTGGGCTCCAGCCATTCT 479

RESULT 7
US-11-136-527-3691
; Sequence 3691, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3691
; LENGTH: 2348
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3691

Query Match 5.7%; Score 66.6; DB 14; Length 2348;
Best Local Similarity 52.3%; Pred. No. 2.3e-08;
Matches 172; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 46 GTCCCTTGGCATTTTAAATGTCCTGCTGCTTTGCTATACGATAGCATGCTGTG 105
DB 333 GTCTTCAATTTGCCCTTCTTAAACCGGCTTCTTGGCATTTGGTACCATCATTTGGCAACATCCTT 392

QY 106 GTCAATTTTAGCCCTTTCTAGCAGACAGAAACCTTTAGACATCGAAGTAATTTTCTT 165
DB 393 GTCAATTTGGCCCTTCAAGTCAACAACAGCTGACAGACAGTCAACAATCTTCTCTTA 452

QY 166 AATTTGGCTATTTCTGACTTTCTGCTGGGTGTCATCTCCATTCCTCTGTACATCCCTCAC 225
DB 453 AGCTGGCCCTGTGACAGACCTGATCATCGGGGTCAATTTCCATGAACCTGTTCACCTAC 512

QY 226 AGCTGTTTAAAC---TGGAAATTTTGAAGTGGATCTGATGTTTGGCTCATCTAGAC 282
DB 513 ATCAATTAAGAACCGTTGGGCACTTGGGGAATTTAGCCTGCGACCTCTGGCTCTCCATTTGAC 572

QY 283 TATCTTTTGTGACAGACATCCGCTCTACAGTATTGCTCTCATAGCTACGATCGATACCAG 342
DB 573 TATGTGGCAGCAATGCCCTCTGTGCATGANTCTGCTGTATAGCTTTGACAGTACTTT 632

QY 343 TCAGTTTCAAACTGCTGCTTATAGAGC 371
DB 633 TCCATCACTAGGCCCACTCACTACCGAGC 661

RESULT 8
US-11-036-196-1495
; Sequence 1495, Application US/11036196
; Publication No. US20060078900A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory

; APPLICANT: Higgs, Brandon
; APPLICANT: Cattle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/11/036,196
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US/10/152,319
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1495
; LENGTH: 3578
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_012527
US-11-036-196-1495

Query Match 5.7%; Score 66.6; DB 11; Length 3578;
Best Local Similarity 52.3%; Pred. No. 2.9e-08;
Matches 172; Conservative 0; Mismatches 154; Indels 3; Gaps 1;
QY 46 GTCCCTTGGCATTATTAATGTCCTGCTGCTTTGCTATACGATAGGCAATGCTGTG 105
DB 242 GTCTTCAATGCTTCTTAACCTGCTTCCCTGGCATGCTGACCATCATTTGGCAACATCCTT 301
QY 106 GTCAATTTAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAAATATTTTCTT 165
DB 302 GTCATGTGGCCCTTCAAGGTCAACAACAGCTGAGACAGTCAACAATCTTCTCTTCTTA 361
QY 166 AATTTGGCTATTTCTGACTTTCTTGGGGGTGTCATCTCCATTCCTCTGTACATCCCTCAC 225
DB 362 AGCTGGCCCTGTGCAGACCTGATCATCGGGGTCAATTTCCATGAACCTGTTCACTACCTAC 421
QY 226 ACCTGTTTAAAC---TGGAAATTTGGAAGTGAATCTGCAATGTTTGGCTCATCTACTGAC 282
DB 422 ATCATTTGAACCGTTTGGGCACTGCGGGAACCTTAGCCCTGCGACCTCTGGCTCTCCATTCG 481
QY 283 TATCTTTTGGCAGACATCGCTCTACAGTATGCTCTCATTTAGCTACGATCGATACGAC 342
DB 482 TAGTGGCCAGCAATGCTCTGTCAATGAATCTGCTGTCTATCAGCTTTTGACAGGTACTTT 541
QY 343 TCAGTTTCAAAACGCTGTGCGTTATAGAGC 371
DB 542 TCCATCACTAGGCCACTCACTTACCAGC 570

RESULT 9
US-11-136-527-2030
; Sequence 2030, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AMI01086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2030
; LENGTH: 4095
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2030
Query Match 5.7%; Score 66.6; DB 14; Length 4095;
Best Local Similarity 52.3%; Pred. No. 3.1e-08;
Matches 172; Conservative 0; Mismatches 154; Indels 3; Gaps 1;
QY 46 GTCCCTTGGCATTATTAATGTCCTGCTGCTTTGCTATACGATAGGCAATGCTGTG 105
DB 749 GTCTTCAATGCTTCTTAACYGGCTTCCCTGGCATGCTGACCATCATTTGGCAACATCCTT 808
QY 106 GTCAATTTAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAAATATTTTCTT 165
DB 809 GTCAATTTGGCCCTTCAAGGTCAACAACAGCTGAGACAGTCAACAATCTTCTCTTA 868
QY 166 AATTTGGCTATTTCTGACTTTCTTGGGGGTGTCATCTCCATTCCTCTGTACATCCCTCAC 225
DB 869 AGCTGGCCCTGTGCAGACCTGATCATCGGGGTCAATTTCCATGAACCTGTTCACTACCTAC 928
QY 226 ACCTGTTTAAAC---TGGAAATTTGGAAGTGAATCTGCAATGTTTGGCTCATCTACTGAC 282
DB 929 ATCATTTGAACCGTTTGGGCACTGCGGGAACCTTAGCCCTGCGACCTCTGGCTCTCCATTCG 988
QY 283 TATCTTTTGGCAGACATCGCTCTACAGTATGCTCTCATTTAGCTACGATCGATACGAC 342
DB 989 TAGTGGCCAGCAATGCTCTGTCAATGAATCTGCTGTCTATCAGCTTTTGACAGGTACTTT 1048
QY 343 TCAGTTTCAAAACGCTGTGCGTTATAGAGC 371
DB 1049 TCCATCACTAGGCCACTCACTTACCAGC 1077

RESULT 10
US-11-136-527-3114
; Sequence 3114, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AMI01086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3114
; LENGTH: 2633
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3114
Query Match 5.6%; Score 66.4; DB 14; Length 2633;
Best Local Similarity 52.8%; Pred. No. 2.8e-08;
Matches 167; Conservative 0; Mismatches 146; Indels 3; Gaps 1;
QY 69 CCTGCTTGGCTTTTGGCTATACGATAGGCAATGCTGTGCTCATTTTAGCCCTTTGAGCAGA 128
DB 245 CCTCCTGTCTCTAGCTACAGTGACAGGCAACCTTACTGGTACTCATCTCTCTTCAAGGTCAA 304


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; SEQ ID NO 17
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-17

Query Match      4.8%; Score 56.4; DB 14; Length 1773;
Best Local Similarity 50.0%; Pred. No. 1.8e-05;
Matches 169; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

Qy 46 GTCCCTTGGCATTTTAAATGTCCTGCTTGGCTTTTGTCTATACGATAGGCAATGCTGTG 105
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
205 GTCTTCATCGCTTTCTTAAACGGGCATCTGGCCCTGGTGACCATCATCGGCAACATCCTG 264
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
106 GTCAATTTAGCCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTT 165
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
265 GTAAATGTGTCAATTTAAGGTCAACAGCAGCTGAAGACGGGTCAACAACTACTTCCCTCTTA 324
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
166 AATTTGGCTATTTCTGACTTCTTCGTGGGTGTCATCTCCATCTCTGTACATCCCTCAC 225
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
325 AGCTGCTCTGTCGGATCTGAATATCGGGGTCAATTTCAATGAATCTGTTTACGACCTAC 384
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
226 ACCTGTTTAAAC---TGGAAATTTTGAAGTGGAAATCTGCATGTTTGGCTCATTTACTGAC 282
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
385 ATCATCATGAATCGATGGCCCTTAGGGAACCTTGGCCTGTGACCTCTGGCTTGCCATTGAC 444
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
283 TATCTTTTGTGACAGCATCGCTCTACAGTATGCTCTCATTTAGCTAGCATCGATCGATACGAG 342
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
445 TACGTAGCAGCAATGCTCTGTATGAATCTTCTGGTCTATCAGCTTTTGACAGATACTTT 504
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
343 TCAGTTTCAAACGCTGTGCGTTATAGACACAGCACAC 380
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
505 TCCATCAGAGCGCGCTCAGCTACCGAGCCAAACGAAC 542

RESULT 14
US-11-124-368A-14
; Sequence 14, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1974
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-368A-14

Query Match      4.8%; Score 56.4; DB 14; Length 1974;
Best Local Similarity 50.0%; Pred. No. 1.9e-05;
Matches 169; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

Qy 46 GTCCCTTGGCATTTTAAATGTCCTGCTTGGCTTTTGTATACGATAGGCAATGCTGTG 105
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
205 GTCTTCATCGCTTTCTTAAACGGGCATCTGGCCCTGGTGACCATCATCGGCAACATCCTG 264
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
106 GTCAATTTAGCCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTT 165
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
265 GTAAATGTGTCAATTTAAGGTCAACAGCAGCTGAAGCGGTCAACAACTACTTCTCTTA 324
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
166 AATTTGGCTATTTCTGACTTCTTCGTGGGTGTCATCTCCATCTCTGTACATCCCTCAC 225
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Db 325 AGCTGCGCTGTGCGGATCTGAATATCGGGGTCAATTTCAATGAATCTGTTTACGACCTAC 384
Qy 226 ACCTGTTTAAAC---TGGAAATTTTGAAGTGGAAATCTGCATGTTTGGCTCATTTACTGAC 282
Db 385 ATCATCATGAATCGATGGCCCTTAGGGAACCTTGGCCCTGTGACCTCTGGCTTTGCCATTGAC 444
Qy 283 TATCTTTTGTGACAGCATCGCTCTACAGTATGCTCTCATTTAGCTAGCATCGATCGATACCGAG 342
Db 445 TACGTAGCAGCAATGCTCTGTATGAATCTTCTGGTCTATCAGCTTTTGACAGATACTTT 504
Qy 343 TCAGTTTCAAACGCTGTGCGTTATAGACACAGCACAC 380
Db 505 TCCATCAGAGCGCGCTCAGCTACCGAGCCAAACGAAC 542

RESULT 15
US-11-136-527-7845
; Sequence 7845, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7845
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-7845

Query Match      4.7%; Score 54.8; DB 14; Length 600;
Best Local Similarity 51.7%; Pred. No. 3.1e-05;
Matches 125; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Qy 884 TGGAGCTTCTCAGAGGCGAGGAAGCTAGCCAGGTGCTAGCTGCTCTCTGAGTGTCTTTG 943
Db 335 TGGCTTGGCCCGTGAAGGAGAGCGTGAAGACTCTGGGCATCATCATATGGCACCTTCA 394
Qy 944 CCATTTGCTGGGCTCCGATTTGCTGTTCAAAATGTTCTTTCAACTTATGCGAGAGGG 1003
Db 395 TCCTCTGCTGGCTGCGCTTTTTCATTGCTGCTCTGCTGCTCTGCTGCTGCTGCTGCT 454
Qy 1004 AGCGCCCAATCGATTTGGTACAGATAGCTTTTGGCTACAGTGGTTCATTTCACTTA 1063
Db 455 GCCACATGCTGCGTTGTTGGGTGCCATAATTAATCTGGCTAGGCTACTTCCAACTCCCTGC 514
Qy 1064 TTAATCCCTTTCTATACCTTTTGGCCACAGAGCTTTCCAGAGGCTTTCTCGAAGATAC 1123
Db 515 TCAATCCGGTTATTTATGCTTATTTCAACAAAGACTTTCAAAAGCGCTTTTAAGAAGATAA 574
Qy 1124 TC 1125
Db 575 TC 576

Search completed: April 29, 2006, 00:18:43
Job time : 690 secs
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Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLY 358
Qy 361 PLCHRRFQKAFWKILCVTKQAPSQ-TQS VSS 391
Db 359 PLCHRRFQKAFWKILCVTKQAPSQHSRSVSS 390
RESULT 2
US-09-812-216-2
; Sequence 2, Application US/09812216
; Patent No. 6613533
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-216-2

Query Match 68.6%; Score 1403.5; DB 2; Length 390;
Best Local Similarity 69.1%; Pred. No. 1.2e-112;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;
Qy 1 MSBSNGTDVLPITAOVPLAFMLSLAFATIGNAVVILAFVADRNLRHRSNYFFFLNLALS 60
Db 1 MPDTNSTINLSLSTRVTLAFMFSLVAFALMGNALVILAFVVDKDLRHRSYFFFLNLALS 60
Qy 61 DFFVGVISIPLYIPHTLFNPNPGSGICMFWLIITDYLLCTASVYSIVLISYDRYQSVSNV 120
Db 61 DFFVGVISIPLYIPHTLFNPNPGSGICMFWLTDTLLCTASVYVNIIVLISYDRYLSVSNV 120
Qy 121 RYRAQHTGILKIVAQVAVWVILAFVNGPMILASDSKNSNTTECEPCGFVTEWYILAIT 180
Db 121 SYRTOHTGVLKIVTLMAVAVVLAFLVNGPMILVSESWKDEGS--ECEPGFFSEWYILAIT 178
Qy 181 AFLEFLLPVSLVVYFSVQIYWSLWKRGSLSRCPSHAGFIATSSRGTHSRRTGLACRTSL 240
Db 179 SFLEFVIPVLIVAFNNIYWSLWKDDHLSRCQSHPGLTAVSNNICGHSFGRGLSRRSL 238
Qy 241 PGLKEPAASLHSPRGKSLLSVLRTHMSGSIAPKVGSCFKSESFVLHQREHVLLRG 300
Db 239 SASTVEVPASHSRQRKSLMSFSSRTKWSNTIASKMGFSQSDSVLHQREHVLLRA 298
Qy 301 RKLARSLAVLLSAFACWAPYCLFTVLTSTYRRGERPKSIWYSIAFWLQWFNSLNPFLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLY 358
Qy 361 PLCHRRFQKAFWKILCVTKQAPSQ-TQS VSS 391
Db 359 PLCHRRFQKAFWKILCVTKQAPSQHSRSVSS 390

RESULT 3
US-09-875-076-14
; Sequence 14, Application US/09875076
; Patent No. 6869776
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.

; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-076-14

Query Match 68.6%; Score 1403.5; DB 2; Length 390;
Best Local Similarity 69.1%; Pred. No. 1.2e-112;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;
Qy 1 MSBSNGTDVLPITAOVPLAFMLSLAFATIGNAVVILAFVADRNLRHRSNYFFFLNLALS 60
Db 1 MPDTNSTINLSLSTRVTLAFMFSLVAFALMGNALVILAFVVDKDLRHRSYFFFLNLALS 60
Qy 61 DFFVGVISIPLYIPHTLFNPNPGSGICMFWLIITDYLLCTASVYSIVLISYDRYQSVSNV 120
Db 61 DFFVGVISIPLYIPHTLFNPNPGSGICMFWLTDTLLCTASVYVNIIVLISYDRYLSVSNV 120
Qy 121 RYRAQHTGILKIVAQVAVWVILAFVNGPMILASDSKNSNTTECEPCGFVTEWYILAIT 180
Db 121 SYRTOHTGVLKIVTLMAVAVVLAFLVNGPMILVSESWKDEGS--ECEPGFFSEWYILAIT 178
Qy 181 AFLEFLLPVSLVVYFSVQIYWSLWKRGSLSRCPSHAGFIATSSRGTHSRRTGLACRTSL 240

Db 179 SFLEFVPIVLVAYFNWNIWLSWKRDHLSRCOSHPLGTAVSSNICGHSFGRGLSSRRSL 238
Qy 241 PGLKEPAASHSESPPGKSLLSVLTRHMSGSIAPKVGSCFCSSESPVTLHQHREVELLRG 300
Db 239 SASTEVPAFSPHRSQRKRSLSMFSRRTKMSNTIASKMGFSQSDSVLHQHREVELLRA 298
Qy 301 RKLARSIAVLISALFALCWAPYCLPTIVLSTYRGERPKSIWYSIAFWLQWNSLINPFY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSUFTIVLSFYSSATGKSVVYRIAFWLQWNSFVNPLLY 358
Qy 361 PLCHRRFQKAFWKILCTVKQAPSQ-TQSVSS 391
Db 359 PLCHKRFQAFKIFCIKKQPLSQHSRSVSS 390
RESULT 4
US-10-453-106-2
; Sequence 2, Application US/10453106
; Patent No. 6906060
; GENERAL INFORMATION:
; APPLICANT: Peschke, Bernd
; APPLICANT: Hohlweg, Rolf
; TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-A]PYRAZINES,
; TITLE OF INVENTION: OCTAHYDROPYRIDO[1,2-A]PYRAZINES AND
; TITLE OF INVENTION: DECAHYDROPIRAZINO[1,2-A]AZEPINES
; FILE REFERENCE: 6483.200-US
; CURRENT APPLICATION NUMBER: US/10/453,106
; CURRENT FILING DATE: 2003-06-03
; PRIOR FILING DATE: 2003-06-07
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Monkey
US-10-453-106-2

Query Match 34.1%; Score 698; DB 2; Length 445;
Best Local Similarity 37.8%; Pred. No. 5.8e-52;
Matches 165; Conservative 49; Mismatches 126; Indels 96; Gaps 11;
Qy 18 LAFMSLLAPAITIGNAVILAFVADNRNLHRSNYFNLNLAISDPFVGVISIPLYIPHTL 77
Db 37 LAALMALLIVATVGLGNALVMAFVADSSLRQTQNNFFLNLAISDFLVGAFCIPLYVYVYL 96
Qy 78 F-NWNPSSGICMPWLITDYLLCTASVYSIVLISYDRYQSVSNVRAQHTGILKIVAOM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLISYDRPLSVTRAVSYRAQQNTTRAVRK 156
Qy 137 VAWVILAFVNGPMILASDWSK-----NSTNTECEPFGFVTEWYILAITAFLEFLPVSL 191
Db 157 LLVWVLAFLYLGPAIL---SWEYLSGSSIPGHCYAEFPYNYFLITASTLEFFTPFLS 213
Qy 192 VYFVSQIY-----NSLWKGSLSRCPSH 215
Db 214 VTFPNLSIYLNIOQRTLRDLGAREAGPEPPPEAQPSPPPPGCGWCKGHEAMPLH 273
Qy 216 -----AGFIATSSRGTHSRRTGLACTSLPGLKEPAASHSESPPGKSLLV 263
Db 274 RYGVGBAAAGAEAGETALGGGGGGS-----AASPTSSG-----SSRGTERRP 318
Qy 264 SLRTHMSGSIAPKVGSCFCSSESPVTLHQ-----EHVELLRGKRLARSIAVLISAF 314
Db 319 -----SLKRGSKPSSASSLEKRMKMSVQSPTQRFRLSRDRKVAKSIAVVISIF 367
Qy 315 AICWAPYCLPTIVLSTYRGERPKSIWYSIAFWLQWNSLINPFYPLCHRRFQKAFWKI 374
Db 368 GLCWAPYLLMITRAAC-HGHCVPDYWYETSFLLWANSVAVNPVLPCLCHHSFRFAFTKL 426

Qy 375 LCVTK---OPAPSQTQ 387
Db 427 LCPQKLIKQPHSLEQ 442
RESULT 5
US-08-985-090-2
; Sequence 2, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-985-090-2

Query Match 33.9%; Score 693; DB 1; Length 445;
Best Local Similarity 37.6%; Pred. No. 1.6e-51;
Matches 163; Conservative 50; Mismatches 124; Indels 96; Gaps 11;
Qy 18 LAFMSLLAPAITIGNAVILAFVADNRNLHRSNYFNLNLAISDPFVGVISIPLYIPHTL 77
Db 37 LAALMALLIVATVGLGNALVMAFVADSSLRQTQNNFFLNLAISDFLVGAFCIPLYVYVYL 96
Qy 78 F-NWNPSSGICMPWLITDYLLCTASVYSIVLISYDRYQSVSNVRAQHTGILKIVAOM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLISYDRPLSVTRAVSYRAQQNTTRAVRK 156
Qy 137 VAWVILAFVNGPMILASDWSK-----NSTNTECEPFGFVTEWYILAITAFLEFLPVSL 191
Db 157 LLVWVLAFLYLGPAIL---SWEYLSGSSIPGHCYAEFPYNYFLITASTLEFFTPFLS 213
Qy 192 VYFVSQIY-----NSLWKGSLSRCPSH 215
Db 214 VTFPNLSIYLNIOQRTLRDLGAREAGPEPPPEAQPSPPPPGCGWCKGHEAMPLH 273
Qy 216 -----AGFIATSSRGTHSRRTGLACTSLPGLKEPAASHSESPPGKSLLV 263
Db 274 RYGVGBAAAGAEAGETALGGGGGGS-----VASPTSSG-----SSRGTERRP 318
Qy 264 SLRTHMSGSIAPKVGSCFCSSESPVTLHQ-----EHVELLRGKRLARSIAVLISAF 314
Db 319 -----SLKRGSKPSSASSLEKRMKMSVQSPTQRFRLSRDRKVAKSIAVVISIF 367

Qy	137	VAVWILAFVNGPMIIASDWSK-----NSTNTEECBPGFTWTWYIILAIATAFLFLLPVSL	191
Db	161	LLVWVLAFLLYPAIL--SWEYLGGSSIPBGCHVCBAEFYNWYFLITASTLFEFFPFLS	217
Qy	192	VVYESVQIY-----WSLMKRGSLSRCPSH	215
Db	218	VTFFNLSTLYLNIORETRULKDGAEEAGPEPPPEAQSPPPPCCGCGCWKGHGEAMPLH	277
Qy	216	-----AGFIATSSRTGHSRRTGLACRTSLPLCKEPAASLSHSESPRGKSLLV	263
Db	278	RYGUGEAANGVAEGRATLCGGGGGGGS-----VASPTSSG-----SSRGTERPR-----	322
Qy	264	SLRTHMSGSIITAFKVGSFCRSSESPVLHOR-----EHVELLRGRKLARSLAVLLSAF	314
Db	323	-----SLKSGSPSASSASLEKMKMVSQSFTORFRLSDRKVKAKSLAVIVSIF	371
Qy	315	AICWAPYCLFTIVLSTRGERPKSIWYSIAFWLOWNSLINPFYPLCHRRFQKAFWKI	374
Db	372	GLCWAPYTLLMIIRAAC-HGHCVDPWYVETSPWLLWANSAVPVLPYLCHSHSFRAFTKI	430
Qy	375	LCVTYK---QPAPS	384
Db	431	LCPOKLTQPHSS	443

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RESULT 13
US-09-891-053-20
; Sequence 20, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; FILE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-891-053-20

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Query Match	33.9%;	Score 693;	DB 2;	Length 453;
Best Local Similarity	37.6%;	Pred. No. 1.6e-51;		
Matches	163;	Conservative 50;	Mismatches 124;	Indels 96;
Gaps	11;			
Qy	18	LAFIWSLLAFATITIGNAVVILAFVADRNLRHSVFFLNLAISDPFVGVISIPLYIPIHTL	77	
Db	37	LAALMALLIVATVIGNALVULAFVADSGSLRTQNNFFLLNLAISDFLVGAFCIPLYIPVVL	96	
Qy	78	F-NNPQSGICMFWLITDYLCTASVYSIVLISYDRQYSVSNVARYRAQHTGILKIQAQM	136	
Db	97	TGRWTFGRGLCKLWLWVDYLLCTSSAFNVILISYDRFLSVTRAVSYRAQQGDTERRAVKRM	156	
Qy	137	VAVWILAFVNGPMILASDSWK-----NSTWTECEPCFVTEWILAITAFLELLPVSL	191	
Db	157	LLVWVLAFLLYGPAIL---SWEYLSGSSSIPEGHCYAEFFVNNYFLTITASTLEFTTFPLS	213	
Qy	192	VVYFSVQIY-----WSLWKRGISLRCPFSH	215	

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Db 214 VTFFNLSTYLNIOQRTRLRLLDCAEEAAGPEPPPEAQPSPPPPGCGCWQKGHGGEAMPLH 273
QY 216 -----AGFIATSSRGTHSRRTGLACRTSLPGLKEPAASLHSESPRGKSSLIV 263
Db 274 RYGVGEAAVGAEGATLGGGGGGS-----VASPTSSG-----SSRGTGTERPR----- 318
QY 264 SLRTHMSGSIIAFKVGSFCRSESPVLHOR-----EHVELLRGRKLARS LAVLLSAF 314
Db 319 -----SLKSGSKPSASSASLEKRMKMSQSFQRFSLSDRKVAKSLAIVISIF 367
QY 315 AICWAPYCLFTIVISTYRGRBRPKSIWYSIAFWLQWNSLINPFYIPICHRRFQKAFWKI 374
Db 368 GLCWAPYTLMIIRAAC-HGHCVPDYMWYETSFLLWANSVNPVLYPLCHHSFRFAATKL 426
QY 375 LCVTK---QAPAS 384
Db 427 LCPQKLTIQPHSS 439

RESULT 14
US-09-891-053-1
; Sequence 1, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohka, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-891-053-1

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Query Match	33.7%	Score 690;	DB 2;	Length 413;
Best Local Similarity	38.6%;	Pred. No. 2.6e-51;		
Matches 160; Conservative	48;	Mismatches 121;	Indels 86;	Gaps 10;
Qy	18	LAFWMSLLAFATTTGNAAVWILAFVADRNLRHRSNVFFLNLAISDFPFGVIGVSIPLVPIHTL	77	
Db	37	LAALMLLIIVATVLGNALVWLAFFVADSSRLTQNNFFLLNLAISDFLVGAFCIPLYVPVL	96	
Qy	78	F-NNPQSGICMFWLITDYLLCTASVSVILSYDQYQSVNAVRYRAQHTGIILKIVAQM	136	
Db	97	TGRWTFGRGLCKLWLVADYLLCASSVFNILSYDRLSVTRAVSYRAQQDTRRAVRKM	156	
Qy	137	VAVWILAFVNGPMILASDSWK-----NSTNTECEPGFTWETWILAITATLEFLLPVSL	191	
Db	157	ALVWVLAFLLYGPAIL---SWEYLGSGSSIDEGHCYAEFFVNNVFLTASTLEFPTFLS	213	
Qy	192	VVYFSVQIY-----WSLWTKGSLSRCPSH	215	
Db	214	VTFFNLSTYLNIQRRTRLRDGCGREAGPEPPDQAQPPPPAPPSCWCPKPGHCEAMPLH	273	
Qy	216	AGFIATSGRGTHGRRTGLACRTSLPGLKBPAAASHSESPPGKSSLLVSLRTHMSGIIA	275	

Db 274 SS--GSSSRGTERPR-----SLKRGSKPSASSASLEKRMKM-----VSQSI-- 312
QY 276 FKVGSCRSFVHLQREHVELLRGRKLARSALVLSAFAICWAPYCLFTIVLSTYRRGE 335
Db 313 -----TQFRLSRDKKVKAKSLAIIIVSIFGLCWAPYLLMIIRAAC-HGR 355
QY 336 RPKSIWYSIAFWLQWNSLINPPLYPCHRRRFQKAFWKILCVTK---QPAPSQQTQ 387
Db 356 CIPDYWYETSPWLLWANSVNPVLYPLCHYSFRRAFTKLLCPQKLKVQPHGSLEQ 410

RESULT 15

US-09-165-543-5
; Sequence 5, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-165-543-5

Query Match 33.3%; Score 682; DB 2; Length 445;
Best Local Similarity 37.0%; Pred. No. 1.4e-50;
Matches 160; Conservative 51; Mismatches 133; Indels 88; Gaps 10;

QY 18 LAPLSLLAFATIGNAVILAFVADRNLRHSNYFFLMLAISDFVGVISIPLYIPHTL 77
Db 37 LAALMALLIVATVIGNALVMAFVADSLRTQNFLLNLAISDFLVGAFCIPLYVYPVL 96
QY 78 F-NWNPFGSICMFMLITDVLCTPASVYIVLISYDRYQSVNARYRAOHTGILKIVQM 136
Db 97 TGRWTFGRGLCKULWLVVDVLLCCASSVFNIVLSYDRFLSVTRAVSYRAOQDTRRAVRKM 156
QY 137 VAVWILAFVNGPMILASDSWK-----NSTNTECEPGFVTEWYIILAITAFLEFLLPVSL 191
Db 157 ALVWVLAFLLYGPAIL---SWEVLSGSSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLS 213
QY 192 VYVFSVQIY-----WSLWKRGSLSRCPSH 215
Db 214 VTFFNLSTIYLNIOQRTRLLDGGREAGBPDPDQAPSPPPAPPCWCWPKHGHEAMPLH 273

QY 216 AGFIATSRGT-----GHSRRRTGLACRTSLPGLKEPAASLHSESPPKSGSLLVSLRT 267
Db 274 RYGVGEAGVGEAGEAALGGSGGGAASPTSSG-----SSRGTGTERPR----- 318
QY 268 HMSGIIIAFKVGSFCRSFSPVLHQR-----EHVELLRGRKLARSALVLSAFAICW 318
Db 319 -----SLKRGSKPSASSASLEKRMKMVSQSIQFRFLSRDKKVKAKSLAIIIVSIFGLCW 371
QY 319 APYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLINPPLYPCHRRRFQKAFWKILCVT 378
Db 372 APYTLMIIRAAC-HGRCPDYWYETSPWLLWANSVNPVLYPLCHYSFRRAFTKLLCPQ 430
QY 379 K---QPAPSQQTQ 387
Db 431 KLVQPHGSLEQ 442

Search completed: April 26, 2006, 20:47:41
Job time : 29 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 26, 2006, 20:57:34 ; Search time 163 Seconds
(without alignments)
1002.278 Million cell updates/sec

Title: US-10-626-126-9
Perfect score: 2045
Sequence: 1 MSESNGTDVLPITAQVPLAF.....WKILCVTKQAPSQTSQVS 391

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pap:*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pap:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pap:*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pap:*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pap:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2045	100.0	391	5	US-10-626-445-9
2	2045	100.0	391	5	US-10-626-126-9
3	2045	100.0	391	5	US-10-626-398-9
4	1735	84.8	391	5	US-10-626-445-8
5	1735	84.8	391	5	US-10-626-126-8
6	1735	84.8	391	5	US-10-626-398-8
7	1403.5	68.6	390	3	US-09-812-216-2
8	1403.5	68.6	390	3	US-09-910-411-2
9	1403.5	68.6	390	3	US-09-875-076-14
10	1403.5	68.6	390	3	US-09-876-252-14
11	1403.5	68.6	390	3	US-09-852-165-2
12	1403.5	68.6	390	3	US-09-891-138A-6
13	1403.5	68.6	390	4	US-10-052-193-2
14	1403.5	68.6	390	4	US-10-225-567A-629
15	1403.5	68.6	390	4	US-10-272-983-14
16	1403.5	68.6	390	4	US-10-354-769-2
17	1403.5	68.6	390	4	US-10-393-807-14
18	1403.5	68.6	390	4	US-10-417-820A-14
19	1403.5	68.6	390	4	US-10-349-253A-2
20	1403.5	68.6	390	4	US-10-696-673-2
21	1403.5	68.6	390	4	US-10-723-955-14
22	1403.5	68.6	390	4	US-10-782-596-14
23	1403.5	68.6	390	4	US-10-737-619-2
24	1403.5	68.6	390	5	US-10-626-445-2
25	1403.5	68.6	390	5	US-10-684-206-20
26	1403.5	68.6	390	5	US-10-816-088-2
27	1403.5	68.6	390	5	US-10-626-126-2

28	1403.5	68.6	390	5	US-10-626-398-2	Sequence 2, Appli
29	1403.5	68.6	390	5	US-10-756-149-4702	Sequence 4702, Ap
30	1403.5	68.6	390	5	US-10-723-955-14	Sequence 14, Appl
31	1403.5	68.6	390	5	US-10-488-421-8	Sequence 8, Appli
32	1398.5	68.4	390	4	US-10-290-078-27	Sequence 27, Appl
33	1398.5	68.4	390	5	US-10-488-421-6	Sequence 6, Appli
34	1236.5	60.5	389	5	US-10-626-445-10	Sequence 10, Appl
35	1236.5	60.5	389	5	US-10-626-126-10	Sequence 10, Appl
36	1236.5	60.5	389	5	US-10-626-398-10	Sequence 10, Appl
37	1233	60.3	357	5	US-10-488-421-4	Sequence 4, Appli
38	1117.5	54.6	336	5	US-10-488-421-2	Sequence 2, Appli
39	698	34.1	445	4	US-10-453-106-2	Sequence 2, Appli
40	698	34.1	445	5	US-10-735-963-2	Sequence 2, Appli
41	693	33.9	445	3	US-09-350-206-2	Sequence 2, Appli
42	693	33.9	445	3	US-09-349-755-2	Sequence 2, Appli
43	693	33.9	445	3	US-09-166-334-2	Sequence 2, Appli
44	693	33.9	445	4	US-10-282-958-2	Sequence 2, Appli
45	693	33.9	445	4	US-10-225-567A-549	Sequence 549, App

ALIGNMENTS

RESULT 1
US-10-626-445-9
; Sequence 9, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-626-445-9

Query Match	100.0%;	Score 2045;	DB 5;	Length 391;
Best Local Similarity	100.0%;	Pred. No. 1.2e-183;		
Matches	391;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MSESNGTDVLPITAQVPLAFPLMSLLAFATITIGNAVVILAFVADRNLRHRSNYFFLNLAIS	60	
Db	1	MSESNGTDVLPITAQVPLAFPLMSLLAFATITIGNAVVILAFVADRNLRHRSNYFFLNLAIS	60	
Qy	61	DFPVGVISPLYPHTLFWNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVNAV	120	
Db	61	DFPVGVISPLYPHTLFWNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVNAV	120	
Qy	121	RYRAQHTGILKIVAQNVAVVILAFVNGPMLASDSWKSTNTEECBPGFVTEWYILAIT	180	
Db	121	RYRAQHTGILKIVAQNVAVVILAFVNGPMLASDSWKSTNTEECBPGFVTEWYILAIT	180	
Qy	181	AFLEFLLPVSVVYFVSQIYWSLWKRGSLRCPESHAGFIATSRGTGHSRRTGLACRTSL	240	
Db	181	AFLEFLLPVSVVYFVSQIYWSLWKRGSLRCPESHAGFIATSRGTGHSRRTGLACRTSL	240	
Qy	241	PGLKEPAAASHSESPRKSSLLVSLRTHMSGSLIAFKVGSFCRSESFPVLQREHVELLRG	300	
Db	241	PGLKEPAAASHSESPRKSSLLVSLRTHMSGSLIAFKVGSFCRSESFPVLQREHVELLRG	300	
Qy	301	RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQFNLSINPFLY	360	
Db	301	RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQFNLSINPFLY	360	

QY 361 PLCHRRFQAFWKILCVTKQAPAPSTQSVSS 391
Db 361 PLCHRRFQAFWKILCVTKQAPAPSTQSVSS 391

RESULT 2

US-10-626-126-9
; Sequence 9, Application US/10626126
; Publication No. US20050074770A1

; GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy

; APPLICANT: Liu, Changlu

; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype

; FILE REFERENCE: PRD-0033

; CURRENT APPLICATION NUMBER: US/10/626,126

; CURRENT FILING DATE: 2003-07-23

; PRIOR APPLICATION NUMBER: 09/790,849

; PRIOR FILING DATE: 2001-02-22

; PRIOR APPLICATION NUMBER: 60/208,260

; PRIOR FILING DATE: 2000-05-31

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 9

; LENGTH: 391

; TYPE: PRT

; ORGANISM: Rattus rattus

US-10-626-126-9

Query Match 100.0%; Score 2045; DB 5; Length 391;

Best Local Similarity 100.0%; Pred. No. 1.2e-183;

Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSESNGTDVLP LTAQVPLAFLMSLLAFPAITIGNAVVILAFVADRNLRHRSNTFFFLNLALS 60
Db 1 MSESNGTDVLP LTAQVPLAFLMSLLAFPAITIGNAVVILAFVADRNLRHRSNTFFFLNLALS 60

QY 61 DFFVGVISITPLYPHTLFNNPFGSGICMPFLITDYLCTASVVISVILISYDRYQSVNAV 120
Db 61 DFFVGVISITPLYPHTLFNNPFGSGICMPFLITDYLCTASVVISVILISYDRYQSVNAV 120

QY 121 RYRAQHTGILKIVAQMVAVWILAFVNGPMLASDSKNSNTTECEPGFVTEWYILAIT 180
Db 121 RYRAQHTGILKIVAQMVAVWILAFVNGPMLASDSKNSNTTECEPGFVTEWYILAIT 180

QY 181 AFLEFLLPVSLVYFSVQIYWSLWKRGSLRCPSHAGFIATSSRGTHSRRTGLACRTSL 240
Db 181 AFLEFLLPVSLVYFSVQIYWSLWKRGSLRCPSHAGFIATSSRGTHSRRTGLACRTSL 240

QY 241 PGLKEPAASLHSESPRGKSLVSLRTHMSGSIIFAPKVSFCRSBPVLHQREHVLELLRG 300
Db 241 PGLKEPAASLHSESPRGKSLVSLRTHMSGSIIFAPKVSFCRSBPVLHQREHVLELLRG 300

QY 301 RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWFNSLINPFLY 360
Db 301 RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWFNSLINPFLY 360

QY 361 PLCHRRFQAFWKILCVTKQAPAPSTQSVSS 391
Db 361 PLCHRRFQAFWKILCVTKQAPAPSTQSVSS 391

RESULT 3

US-10-626-398-9

; Sequence 9, Application US/10626398

; Publication No. US20050074841A1

; GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy

; APPLICANT: Liu, Changlu

; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype

; FILE REFERENCE: PRD-0034

; CURRENT APPLICATION NUMBER: US/10/626,398

; CURRENT FILING DATE: 2003-07-23

; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 9

; LENGTH: 391

; TYPE: PRT

; ORGANISM: Rattus rattus

US-10-626-398-9

Query Match 100.0%; Score 2045; DB 5; Length 391;

Best Local Similarity 100.0%; Pred. No. 1.2e-183;

Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSESNGTDVLP LTAQVPLAFLMSLLAFPAITIGNAVVILAFVADRNLRHRSNTFFFLNLALS 60
Db 1 MSESNGTDVLP LTAQVPLAFLMSLLAFPAITIGNAVVILAFVADRNLRHRSNTFFFLNLALS 60

QY 61 DFFVGVISITPLYPHTLFNNPFGSGICMPFLITDYLCTASVVISVILISYDRYQSVNAV 120
Db 61 DFFVGVISITPLYPHTLFNNPFGSGICMPFLITDYLCTASVVISVILISYDRYQSVNAV 120

QY 121 RYRAQHTGILKIVAQMVAVWILAFVNGPMLASDSKNSNTTECEPGFVTEWYILAIT 180
Db 121 RYRAQHTGILKIVAQMVAVWILAFVNGPMLASDSKNSNTTECEPGFVTEWYILAIT 180

QY 181 AFLEFLLPVSLVYFSVQIYWSLWKRGSLRCPSHAGFIATSSRGTHSRRTGLACRTSL 240
Db 181 AFLEFLLPVSLVYFSVQIYWSLWKRGSLRCPSHAGFIATSSRGTHSRRTGLACRTSL 240

QY 241 PGLKEPAASLHSESPRGKSLVSLRTHMSGSIIFAPKVSFCRSBPVLHQREHVLELLRG 300
Db 241 PGLKEPAASLHSESPRGKSLVSLRTHMSGSIIFAPKVSFCRSBPVLHQREHVLELLRG 300

QY 301 RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWFNSLINPFLY 360
Db 301 RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWFNSLINPFLY 360

QY 361 PLCHRRFQAFWKILCVTKQAPAPSTQSVSS 391
Db 361 PLCHRRFQAFWKILCVTKQAPAPSTQSVSS 391

RESULT 4

US-10-626-445-8

; Sequence 8, Application US/10626445

; Publication No. US20040248252A1

; GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy

; APPLICANT: Liu, Changlu

; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype

; FILE REFERENCE: PRD-0032

; CURRENT APPLICATION NUMBER: US/10/626,445

; CURRENT FILING DATE: 2003-07-23

; PRIOR APPLICATION NUMBER: 09/790,849

; PRIOR FILING DATE: 2001-02-22

; PRIOR APPLICATION NUMBER: 60/208,260

; PRIOR FILING DATE: 2000-05-31

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 8

; LENGTH: 391

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-626-445-8

Query Match 84.8%; Score 1735; DB 5; Length 391;

Best Local Similarity 84.7%; Pred. No. 1.7e-154;

Matches 331; Conservative 17; Mismatches 43; Indels 0; Gaps 0;

QY 1 MSESNGTDVLP LTAQVPLAFLMSLLAFPAITIGNAVVILAFVADRNLRHRSNTFFFLNLALS 60


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Db      1 MSESNTGILPPAAQVPLAFLMSFAPAFIMVGNVILAFVVDNRNLRHRSNYFFLNLAIS 60
Qy      61 DFPVGVISPLYIPHTLFNNPGSGICMFWLITDYLLCTASVYVILISYDRYQSVNAV 120
Db      61 DFLVGLISPLYIPHYLFNNFGSGICMFWLITDYLLCTASVYVILISYDRYQSVNAV 120
Qy     121 RYRAOHTGILKIVAQWAVVILAFVNGPMLASDSWKNSNTTECEPGFVTEWYILAIT 180
Db     121 SYRAOHTGIMKIVAQWAVVILAFVNGPMLASDSWKNSNTTKDCEPGFVTEWYILAIT 180
Qy     181 AFLEFLLPVSLVYVFSQIYWSLWKGSLSRCPESHAGFIATSSRGTHGSHRRRTGLACTSL 240
Db     181 MLLEFLLPVISVAYFNVQIYWSLWKKRALSRCPESHAGFSTSSASGHLHRAGVACRTSN 240
Qy     241 PGLKEPAASLHSPRGKSSLLVSLRTHMSGSIAPKVGSPFCSESPVHLQREHVELLRG 300
Db     241 PGLKESAAASHSPRGKSSILVSLRTHMNSSITAFKVGSESAALRQREYAEALLRG 300
Qy     301 RKLARSLAVLLSAFALCWAPYCLFTTIVLSTYRGERPKSIWYSIAFWLQWNSLNPFLY 360
Db     301 RKLARSLAILLSAFALCWAPYCLFTTIVLSTYRTERPKSVYVYSIAFWLQWNSFVNPFY 360
Qy     361 PLCHRRFQAFWKILCVTKOPAPSOQSVSS 391
Db     361 PLCHRRFQAFWKILCVTKWPALSONQSVSS 391
```

RESULT 5

```
US-10-626-126-8
; Sequence 8, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-626-126-8
```

```
Query Match      84.8%; Score 1735; DB 5; Length 391;
Best Local Similarity 84.7%; Pred. No. 1.7e-154;
Matches 331; Conservative 17; Mismatches 43; Indels 0; Gaps 0;
```

```
Qy      1 MSESNTDVLPLTAQVPLAFLMSLLAFATIGNAVVILAFVADNRNLRHRSNYFFLNLAIS 60
Db      1 MSESNTGILPPAAQVPLAFLMSFAPAFIMVGNVILAFVVDNRNLRHRSNYFFLNLAIS 60
Qy     61 DFPVGVISPLYIPHTLFNNPGSGICMFWLITDYLLCTASVYVILISYDRYQSVNAV 120
Db     61 DFLVGLISPLYIPHYLFNNFGSGICMFWLITDYLLCTASVYVILISYDRYQSVNAV 120
Qy     121 RYRAOHTGILKIVAQWAVVILAFVNGPMLASDSWKNSNTTECEPGFVTEWYILAIT 180
Db     121 SYRAOHTGIMKIVAQWAVVILAFVNGPMLASDSWKNSNTTKDCEPGFVTEWYILAIT 180
Qy     181 AFLEFLLPVSLVYVFSQIYWSLWKGSLSRCPESHAGFIATSSRGTHGSHRRRTGLACTSL 240
Db     181 MLLEFLLPVISVAYFNVQIYWSLWKKRALSRCPESHAGFSTSSASGHLHRAGVACRTSN 240
Qy     241 PGLKEPAASLHSPRGKSSLLVSLRTHMSGSIAPKVGSPFCSESPVHLQREHVELLRG 300
```

```
Db     241 PGLKESAAASHSPRGKSSILVSLRTHMNSSITAFKVGSESAALRQREYAEALLRG 300
Qy     301 RKLARSLAVLLSAFALCWAPYCLFTTIVLSTYRGERPKSIWYSIAFWLQWNSLNPFLY 360
Db     301 RKLARSLAILLSAFALCWAPYCLFTTIVLSTYRTERPKSVYVYSIAFWLQWNSFVNPFY 360
Qy     361 PLCHRRFQAFWKILCVTKOPAPSOQSVSS 391
Db     361 PLCHRRFQAFWKILCVTKWPALSONQSVSS 391
```

RESULT 6

```
US-10-626-398-8
; Sequence 8, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-626-398-8
```

```
Query Match      84.8%; Score 1735; DB 5; Length 391;
Best Local Similarity 84.7%; Pred. No. 1.7e-154;
Matches 331; Conservative 17; Mismatches 43; Indels 0; Gaps 0;
```

```
Qy      1 MSESNTDVLPLTAQVPLAFLMSLLAFATIGNAVVILAFVADNRNLRHRSNYFFLNLAIS 60
Db      1 MSESNTGILPPAAQVPLAFLMSFAPAFIMVGNVILAFVVDNRNLRHRSNYFFLNLAIS 60
Qy     61 DFPVGVISPLYIPHTLFNNPGSGICMFWLITDYLLCTASVYVILISYDRYQSVNAV 120
Db     61 DFLVGLISPLYIPHYLFNNFGSGICMFWLITDYLLCTASVYVILISYDRYQSVNAV 120
Qy     121 RYRAOHTGILKIVAQWAVVILAFVNGPMLASDSWKNSNTTECEPGFVTEWYILAIT 180
Db     121 SYRAOHTGIMKIVAQWAVVILAFVNGPMLASDSWKNSNTTKDCEPGFVTEWYILAIT 180
Qy     181 AFLEFLLPVSLVYVFSQIYWSLWKGSLSRCPESHAGFIATSSRGTHGSHRRRTGLACTSL 240
Db     181 MLLEFLLPVISVAYFNVQIYWSLWKKRALSRCPESHAGFSTSSASGHLHRAGVACRTSN 240
Qy     241 PGLKEPAASLHSPRGKSSLLVSLRTHMSGSIAPKVGSPFCSESPVHLQREHVELLRG 300
Db     241 PGLKESAAASHSPRGKSSILVSLRTHMNSSITAFKVGSESAALRQREYAEALLRG 300
Qy     301 RKLARSLAVLLSAFALCWAPYCLFTTIVLSTYRGERPKSIWYSIAFWLQWNSLNPFLY 360
Db     301 RKLARSLAILLSAFALCWAPYCLFTTIVLSTYRTERPKSVYVYSIAFWLQWNSFVNPFY 360
Qy     361 PLCHRRFQAFWKILCVTKOPAPSOQSVSS 391
Db     361 PLCHRRFQAFWKILCVTKWPALSONQSVSS 391
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RESULT 7

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US-09-812-216-2
; Sequence 2, Application US/09812216
; Publication No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
```

```

; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsema, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-216-2

Query Match      68.6%; Score 1403.5; DB 3; Length 390;
Best Local Similarity 69.1%; Pred. No. 2.8e-123;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

QY 1 MSESNGTDVLPITAOVLAFLMSLLAFAITIGNAVVILAFVADRLNRHRSNYFFFLMLAIS 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MPTDNTNLSLSTRVTLAFAFMSLVAFALMGNALVILAFVVDKRLRHRSYFFFLMLAIS 60

QY 61 DFFVGVISIPLYIPHTLFNWPNGSGICMPWLITDYLCTASVYSIVLISYDRYQSVSNV 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 DFFVGVISIPLYIPHTLFNWPNGSGICMPWLITDYLCTASVYNIVLISYDRYLSVSNV 120

QY 121 RYRAOHTGILKIVAOVAVIILAFVNGPMLIASDKNSNTTECEPGFVTEWYILAIT 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 SRTQHTGVLKIVLMAVAVIILAFVNGPMLIVSVSWKDEGS--ECEPGFFSEWYILAIT 178

QY 181 AFLEFLLPVSLVYVFSQIYWSLWKRGSLRCPSHAGFIATSSRGTHSRRRTGLACRTSL 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 179 SFLEFVIPVLVAYFNMMIYWSLWKRDHLRCQSHPLGLTAVSSNICGHSFRGLSSRRSL 238

QY 241 POLKEPAASLHSESPRGKSSLLVSRTHMSGIILAFKVGSCFSESPVLHQREHVLELRLG 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 239 SASTEPASPFSHERQRKSSLMFSSRTKMNSNTIASKMGSPSQSDSVALHQREHVLELRA 298

QY 301 RLARSLAVLLSAPAI CWAPYCLFTVLSTYRRGERPKSIWYSIAFWLQWNSLNPFLY 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 299 RRLAKSLAILLGVAFCWAPYSLFTVLVSFYSSATGPKSVWYRIAFWLQWNSFVNPLLY 358

QY 361 PLCHRRFQKAFWKILCVTKQAPSQ-TQSVSS 391
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 359 PLCHRRFQKAFWKILCVTKQAPSQ-TQSVSS 390

RESULT 8
US-09-910-411-2
; Sequence 2, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergema, Derek
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
;

; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-910-411-2

Query Match      68.6%; Score 1403.5; DB 3; Length 390;
Best Local Similarity 69.1%; Pred. No. 2.8e-123;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

QY 1 MSESNGTDVLPITAOVLAFLMSLLAFAITIGNAVVILAFVADRLNRHRSNYFFFLMLAIS 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MPTDNTNLSLSTRVTLAFAFMSLVAFALMGNALVILAFVVDKRLRHRSYFFFLMLAIS 60

QY 61 DFFVGVISIPLYIPHTLFNWPNGSGICMPWLITDYLCTASVYSIVLISYDRYQSVSNV 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 DFFVGVISIPLYIPHTLFNWPNGSGICMPWLITDYLCTASVYNIVLISYDRYLSVSNV 120

QY 121 RYRAOHTGILKIVAOVAVIILAFVNGPMLIASDKNSNTTECEPGFVTEWYILAIT 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 SRTQHTGVLKIVLMAVAVIILAFVNGPMLIVSVSWKDEGS--ECEPGFFSEWYILAIT 178

QY 181 AFLEFLLPVSLVYVFSQIYWSLWKRGSLRCPSHAGFIATSSRGTHSRRRTGLACRTSL 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 179 SFLEFVIPVLVAYFNMMIYWSLWKRDHLRCQSHPLGLTAVSSNICGHSFRGLSSRRSL 238

QY 241 POLKEPAASLHSESPRGKSSLLVSRTHMSGIILAFKVGSCFSESPVLHQREHVLELRLG 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 239 SASTEPASPFSHERQRKSSLMFSSRTKMNSNTIASKMGSPSQSDSVALHQREHVLELRA 298

QY 301 RLARSLAVLLSAPAI CWAPYCLFTVLSTYRRGERPKSIWYSIAFWLQWNSLNPFLY 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 299 RRLAKSLAILLGVAFCWAPYSLFTVLVSFYSSATGPKSVWYRIAFWLQWNSFVNPLLY 358

QY 361 PLCHRRFQKAFWKILCVTKQAPSQ-TQSVSS 391
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 359 PLCHRRFQKAFWKILCVTKQAPSQ-TQSVSS 390

RESULT 9
US-09-875-076-14
; Sequence 14, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
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; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-076-14

Query Match      68.6%; Score 1403.5; DB 3; Length 390;
Best Local Similarity 69.1%; Pred. No. 2.8e-123;
Matches 271; Conservative 44; Mismatches 78; Indels 3; Gaps 2;

QY      1  MSESNGDVLPLTAQVPLATLMSLLAFATIGNAVVILAFVADRNLRHRSNYFFLNLAIS 60
DB      1  MPTNSTINISLSTRVTLAFNLSVAFAMLGNALVILAFVDNLRHRSNYFFLNLAIS 60

QY      61  DFFVGVISIPLYPHITLFFNNPGSGICMFPLITDYLCTASVYSIVLISYDRYQSVNAV 120
DB      61  DFFVGVISIPLYPHITLFEWDFGKEICVFWLTIDYLCTASVYVNLVILSYDRYLSVNAV 120

QY      121  RYRAQHTGILKIVAQVAVWILAPLVNGPMLASDSWKNSTNTECEPGFVFWYILAIT 180
DB      121  SYRTQHTGVLIKIVTAVVWVLAFLVNGPMLVSVESWKDEGS--ECEPGFSEWYILAIT 178

QY      181  AFLEPLLPSLVVFSQIVYWSLWKRGSLRCPSHAGFIATSSRGTCHSRBTGLACTSL 240
DB      179  SPLFVPIVTLVAYFNNNIYWSLWKRDHLRSCQSHPLGTAVSSNICGHSFGRLSRRSL 238

QY      241  PGLKEPAASLHRSRPGKSLLSVLRTHMSGSIIAFKVGSFCSRSESPVLHQRHVVELLRG 300
DB      239  SASTEPASFSRQRKSLMSFSSRTKMSNTIASKXGFSQSDSVALHQRHVVELLRA 298

QY      301  RKLARSLAVLSAFAICWAPYCLFTIVLSTRGERPKSIWYSIAFWLQWNSLNPFLY 360
DB      299  RRLAKSLAILLGFAVCWAPYSLFTIVLSPYSSATGPKSVWYRIAFWLQWNSFVNPLLY 358

QY      361  PLCHRFQKAFWKILCVTKOPAFSQ--TQSVSS 391
DB      359  PLCHGRFQKAFKIFCIKKQPLFSQHSRSVSS 390

RESULT 10
US-09-876-252-14
; Sequence 14, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
```

```

; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Kuoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled Rec
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-876-252-14

Query Match      68.6%; Score 1403.5; DB 3; Length 390;
Best Local Similarity 69.1%; Pred. No. 2.8e-123;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

QY 1 MSESNGTDVLP LTAQVPLAFMLSLAPATIGNAVVILAFVADRNLRHRSNYFFFLNLAIS 60
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Db 1 MPDTNSTINLSLSTRVTLAFVMSLVAFAMLGNALVILAFVVDKDLRHRSYFFFLNLAIS 60

QY 61 DFFVGVISIPLYIPHTLFNNPFGSGICMFWLITDYLLCTASVYVILISYDRYQSVNAV 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 DFFVGVISIPLYIPHTLFNDFWDFGKEICVFMLITDYLLCTASVYVILISYDRYLSVNAV 120

QY 121 RYRAQHTGILKIVAQVAVWVILAFVNGPMILASDSWKNSNTTECEPGFVTEWYILAIT 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 SYRTQHTGVLKIVTLMAVWVILAFVNGPMILVSESWKDEGS--ECEPGFFSEWYILAIT 178

QY 181 AFLEFLLPVSLVYFVSQIYWSLWKRGSLRCPSHAGFIATSSRGTHGSHRRRTGLACRTSL 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 179 SFLEFVIPVILVAYFNNIYWSLWKRDHLSCQSHPGELTAVSNSNICGHFRGLSSRRSL 238

QY 241 PGLKEPAASLHSESPRGKSSLLVSLRTHMSGSIIFAFKVGSCFRCSESPVLHQREHVLLRG 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 239 SASTVPASFHSEQRKSSLMFSSRTKNSNTIASKMGSFQSDSDVALHQREHVLLRA 298

QY 301 RKLARSLAVLLSAPALCWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWNSLINPFLY 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLY 358

QY 361 PLCHRRFOKAFWKILCVTKQAPSQ--TQSVSS 391
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Db 359 PLCHRRFOKAFKIFCICKQPLPSQHSRSVSS 390

RESULT 12
US-09-891-138A-6
; Sequence 6, Application US/098911138A
; Publication No. US20030083245A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Daniel Chi-Hong
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030083245A1e1 Receptors
; FILE REFERENCE: 018781-006210US
; CURRENT APPLICATION NUMBER: US/09/891,138A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,461
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR62 G-protein coupled receptor (GPCR)
US-09-891-138A-6

Query Match      68.6%; Score 1403.5; DB 3; Length 390;
Best Local Similarity 69.1%; Pred. No. 2.8e-123;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

QY 1 MSESNGTDVLP LTAQVPLAFMLSLAPATIGNAVVILAFVADRNLRHRSNYFFFLNLAIS 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MPDTNSTINLSLSTRVTLAFVMSLVAFAMLGNALVILAFVVDKDLRHRSYFFFLNLAIS 60

QY 61 DFFVGVISIPLYIPHTLFNNPFGSGICMFWLITDYLLCTASVYVILISYDRYQSVNAV 120
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Db 61 DFFVGVISIPLYIPHTLFNDFWDFGKEICVFMLITDYLLCTASVYVILISYDRYLSVNAV 120

QY 121 RYRAQHTGILKIVAQVAVWVILAFVNGPMILASDSWKNSNTTECEPGFVTEWYILAIT 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 SYRTQHTGVLKIVTLMAVWVILAFVNGPMILVSESWKDEGS--ECEPGFFSEWYILAIT 178

QY 181 AFLEFLLPVSLVYFVSQIYWSLWKRGSLRCPSHAGFIATSSRGTHGSHRRRTGLACRTSL 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 179 SFLEFVIPVILVAYFNNIYWSLWKRDHLSCQSHPGELTAVSNSNICGHFRGLSSRRSL 238

QY 241 PGLKEPAASLHSESPRGKSSLLVSLRTHMSGSIIFAFKVGSCFRCSESPVLHQREHVLLRG 300
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Db 239 SASTVPASFHSEQRKSSLMFSSRTKNSNTIASKMGSFQSDSDVALHQREHVLLRA 298

QY 301 RKLARSLAVLLSAPALCWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWNSLINPFLY 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLY 358

QY 361 PLCHRRFOKAFWKILCVTKQAPSQ--TQSVSS 391
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 359 PLCHRRFOKAFKIFCICKQPLPSQHSRSVSS 390

US-09-852-165-2
; Sequence 2, Application US/09852165
; Publication No. US20030032784A1
; GENERAL INFORMATION:
; APPLICANT: Lind, Peter
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030032784A1e1 G Protein-Coupled Receptors
; FILE REFERENCE: 00231REGUS
; CURRENT APPLICATION NUMBER: US/09/852,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USSN 60/203,108
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-165-2

Query Match      68.6%; Score 1403.5; DB 3; Length 390;
Best Local Similarity 69.1%; Pred. No. 2.8e-123;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

QY 1 MSESNGTDVLP LTAQVPLAFMLSLAPATIGNAVVILAFVADRNLRHRSNYFFFLNLAIS 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MPDTNSTINLSLSTRVTLAFVMSLVAFAMLGNALVILAFVVDKDLRHRSYFFFLNLAIS 60

QY 61 DFFVGVISIPLYIPHTLFNNPFGSGICMFWLITDYLLCTASVYVILISYDRYQSVNAV 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 DFFVGVISIPLYIPHTLFNDFWDFGKEICVFMLITDYLLCTASVYVILISYDRYLSVNAV 120

QY 121 RYRAQHTGILKIVAQVAVWVILAFVNGPMILASDSWKNSNTTECEPGFVTEWYILAIT 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 SYRTQHTGVLKIVTLMAVWVILAFVNGPMILVSESWKDEGS--ECEPGFFSEWYILAIT 178
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Qy 361 PLCHRRFQKAPFKILCVTKQAPSQ-TQSVSS 391
Db 359 PLCHRRFQKAPFKILCVTKQAPSQ-TQSVSS 390

RESULT 13

US-10-052-193-2

; Sequence 2, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-052-193-2

Query Match 68.6%; Score 1403.5; DB 4; Length 390;
Best Local Similarity 69.1%; Pred. No. 2.8e-123;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

Qy 1 MSESNGTDVPLTAQVPLAFMLSLAFATIGNAVVILAFVADRNLRHRSNYFPLNLAIS 60
Db 1 MPDNTNINLSLSTRVTLAFPMFLVAFVAFVADRNLRHRSNYFPLNLAIS 60
Qy 61 DFFVGVISIPLYIPHTLFNWNPGSGICMFWMITDYLCTASVIVLSYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFNWNPGSGICMFWMITDYLCTASVIVLSYDRYQSVNAV 120
Qy 121 RYRAQHTGILKIVAQVAVWILAFVNGPMILASDSWKNSTNTECEPGFVTEWYILAIT 180
Db 121 SYRTOHTGVLKIVTLVAVVWVLAFLVNGPMILVSESWKDEGS--ECEPGFSEWYILAIT 178
Qy 181 AFLEFLPVSLVYVPSQIYVLSLWKGSLRCPSHAGFIATSRGTGHSRRTGLACTSL 240
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Qy 241 PGLKEPAASLHSESPRGKSSLLVSLRTHMSGIIFAFKVGSCFSESPVLHQREHVELLRG 300
Db 239 SASTEVPAFHSERQRRKSSLMFSSRTKMSNTIASKMGFSQSDSVALLHQREHVELLR 298
Qy 301 RKLARSALLSAPAFICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWNSLINPFLY 360
Db 299 RRLAKSAILLGVPAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLNFSVNPFLY 358
Qy 361 PLCHRRFQKAPFKILCVTKQAPSQ-TQSVSS 391
Db 359 PLCHRRFQKAPFKILCVTKQAPSQ-TQSVSS 390

RESULT 14

US-10-225-567A-629
; Sequence 629, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 629
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-629

Query Match 68.6%; Score 1403.5; DB 4; Length 390;
Best Local Similarity 69.1%; Pred. No. 2.8e-123;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

Qy 1 MSESNGTDVPLTAQVPLAFMLSLAFATIGNAVVILAFVADRNLRHRSNYFPLNLAIS 60
Db 1 MPDNTNINLSLSTRVTLAFPMFLVAFVAFVADRNLRHRSNYFPLNLAIS 60
Qy 61 DFFVGVISIPLYIPHTLFNWNPGSGICMFWMITDYLCTASVIVLSYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFNWNPGSGICMFWMITDYLCTASVIVLSYDRYQSVNAV 120
Qy 121 RYRAQHTGILKIVAQVAVWILAFVNGPMILASDSWKNSTNTECEPGFVTEWYILAIT 180
Db 121 SYRTOHTGVLKIVTLVAVVWVLAFLVNGPMILVSESWKDEGS--ECEPGFSEWYILAIT 178
Qy 181 AFLEFLPVSLVYVPSQIYVLSLWKGSLRCPSHAGFIATSRGTGHSRRTGLACTSL 240
Db 179 SFLEFVPIVLVAFYNNIYVLSLWKGSLRCPSHAGFIATSRGTGHSRRTGLACTSL 238
Qy 241 PGLKEPAASLHSESPRGKSSLLVSLRTHMSGIIFAFKVGSCFSESPVLHQREHVELLRG 300
Db 239 SASTEVPAFHSERQRRKSSLMFSSRTKMSNTIASKMGFSQSDSVALLHQREHVELLR 298
Qy 301 RKLARSALLSAPAFICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWNSLINPFLY 360
Db 299 RRLAKSAILLGVPAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLNFSVNPFLY 358
Qy 361 PLCHRRFQKAPFKILCVTKQAPSQ-TQSVSS 391
Db 359 PLCHRRFQKAPFKILCVTKQAPSQ-TQSVSS 390

RESULT 15

US-10-272-983-14
; Sequence 14, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567

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; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-983-14

Query Match      68.6%; Score 1403.5; DB 4; Length 390;
Best Local Similarity 69.1%; Pred. No. 2.8e-123;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

Qy 1 MSESNGTDVLPFTAQVPLAFLMSILLAPAITIGNAVILAFVADRNLRHRSNYFFFLNAIS 60
Db 1 MPDINSTINLSLSTRVTLPFFMSLVAFAPAINLGNALVILAFVVDKNLRHRSYFFFLNAIS 60

Qy 61 DFFVGVISIPLYIPHTLFWNPGSGICMFWLIITDYLLCTASVYSIVLISYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTDTLLCTASVTVNIVLISYDRYLSVNAV 120

Qy 121 RYRAQHTGILKIIVAOVAVVILAFVLNPGMILASDSWKNSTNTTERCEPGFVTEWYILAIT 180
Db 121 SYRTOHTGVLLKIIVLAVVAVLAFVLNPGMILVSESWKDEGS--ECEPGFSEWYILAIT 178

Qy 181 AFLEFLLPVSLVVVFSQIYWSLWKRGSLSRCPSHAGFIATSSRGTGCHSRRTGLACRTSL 240
Db 179 SFLEFVIPVLVYFNNIYWSLWKRDLHLSRQCQSHPGLTAVSSNICGHSPGRLSRRSL 238

Qy 241 PGLKEPAASLHSESPRGKSLVSLRTHMSGSTIAFKVGSFCRSESPVLHQREHVELLRG 300
Db 239 SASTEVPASTHSEQRKKSLSMFSSRTKMSNTIASKMGFSQSQSDSVALHQREHVELLRA 298

Qy 301 RKLARSLAVLSAPACWAPCYCLFTIVLSTYRRGERPKSIWYSIAFWLQWFNSLNPFLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLFQWNSFVNPLLY 358

Qy 361 PLCHRRFQKAFWKILCVTKOPAPSQ-TQSVSS 391
Db 359 PLCHKRFPKAFLLKIFCIKKQLFQSQRSVSS 390
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Search completed: April 26, 2006, 21:01:11
Job time : 165 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 26, 2006, 20:58:38 ; Search time 25 Seconds
(without alignments)
711.274 Million cell updates/sec

Title: US-10-626-126-9
Perfect score: 2045
Sequence: 1 MSSSNGTDVLPFTAQVPLAF.....WKILCVTKQAPASQTQSVS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 232119 seqs, 45477862 residues

Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /SIDSS5/ptodata/2/pubpaa/US08_NEW_PUB_PEP.*
- 2: /SIDSS5/ptodata/2/pubpaa/US06_NEW_PUB_PEP.*
- 3: /SIDSS5/ptodata/2/pubpaa/US07_NEW_PUB_PEP.*
- 4: /SIDSS5/ptodata/2/pubpaa/PCT_NEW_PUB_PEP.*
- 5: /SIDSS5/ptodata/2/pubpaa/US09_NEW_PUB_PEP.*
- 6: /SIDSS5/ptodata/2/pubpaa/US10_NEW_PUB_PEP.*
- 7: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB_PEP.*
- 8: /SIDSS5/ptodata/2/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	698	34.1	445	7	US-11-115-564-2
2	693	33.9	445	7	US-11-115-564-1
3	682	33.3	445	7	US-11-115-564-3
4	594	29.0	441	7	US-11-241-956-3
5	403.5	19.7	590	7	US-11-124-368A-183
6	403.5	19.7	590	7	US-11-127-877-54
7	400	19.6	532	7	US-11-127-877-42
8	395.5	19.3	487	7	US-11-249-847-582
9	361	17.7	466	7	US-11-127-877-41
10	357.5	17.5	429	7	US-11-127-877-51
11	357.5	17.5	466	7	US-11-127-877-50
12	356.5	17.4	480	6	US-10-521-162-40
13	352.5	17.2	400	6	US-10-499-210-2
14	337.5	16.5	450	7	US-11-232-805-26
15	336.5	16.5	450	7	US-11-232-805-27
16	332	16.2	353	6	US-10-875-716-10
17	329	16.1	447	7	US-11-232-805-8
18	328.5	16.1	450	7	US-11-232-805-7
19	321.5	15.7	350	7	US-11-165-024-3
20	306	15.0	365	6	US-10-875-716-9
21	300.5	14.7	446	7	US-11-166-412-67
22	300.5	14.7	462	7	US-11-232-805-44
23	299.5	14.6	477	6	US-10-877-346-47
24	299	14.6	475	6	US-10-877-346-48
25	297.5	14.5	458	7	US-11-232-805-46

26	289.5	14.2	458	6	US-10-877-346-51	Sequence 51, Appl
27	276	13.5	457	6	US-10-877-346-49	Sequence 49, Appl
28	273.5	13.4	440	6	US-10-502-893-2	Sequence 2, Appl
29	273.5	13.4	471	6	US-10-995-561-901	Sequence 901, App
30	272	13.3	269	7	US-11-151-482-5	Sequence 5, Appl
31	270.5	13.2	712	6	US-10-521-162-12	Sequence 12, Appl
32	270	13.2	347	7	US-11-174-816-57	Sequence 57, Appl
33	270	13.2	347	7	US-11-174-819-76	Sequence 76, Appl
34	267.5	13.1	486	6	US-10-877-346-50	Sequence 50, Appl
35	267	13.1	332	7	US-11-174-816-39	Sequence 39, Appl
36	267	13.1	332	7	US-11-174-819-3	Sequence 3, Appl
37	267	13.1	332	7	US-11-217-710-37	Sequence 37, Appl
38	265	13.0	347	7	US-11-174-816-42	Sequence 42, Appl
39	265	13.0	347	7	US-11-174-819-9	Sequence 9, Appl
40	265	13.0	348	7	US-11-174-751-12	Sequence 12, Appl
41	259.5	12.7	349	7	US-11-174-751-22	Sequence 22, Appl
42	254	12.4	348	7	US-11-174-816-11	Sequence 11, Appl
43	247.5	12.1	348	7	US-11-174-816-48	Sequence 48, Appl
44	247.5	12.1	348	7	US-11-174-819-34	Sequence 34, Appl
45	246.5	12.1	345	7	US-11-174-816-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-11-115-564-2
; Sequence 2, Application US/11115564
; Publication No. US20050267116A1
; GENERAL INFORMATION:
; APPLICANT: Peschke, Bernd
; APPLICANT: Hohweg, Rolf
; TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-a]PYRAZINES,
; TITLE OF INVENTION: OCTAHYDROPYRIDO[1,2-a]PYRAZINES AND
; TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-a]AZEPINES
; FILE REFERENCE: 6483.200-US
; CURRENT APPLICATION NUMBER: US/11/115,564
; CURRENT FILING DATE: 2005-04-27
; PRIOR FILING DATE: 2005-04-27
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Monkey
US-11-115-564-2

Query Match	34.1%	Score 698;	DB 7;	Length 445;
Best Local Similarity	37.8%	Pred. No. 4.7e-54;		
Matches	165;	Conservative	49;	Mismatches 126;
				Indels 96;
				Gaps 11;
Qy	18	LAFIMSLAPATIGNAVILAFVADNLRHNRNYFNLNLAISDFVGVISIPLYPHTL	77	
Db	37	LAALMALLIVATIGNALVMAFVADSSLRQNFNLNLAISDFVGVISIPLYPHTL	96	
Qy	78	F-WNPGSGICMFWLITDYLCTASVYSIVLSVDRYOSVNAVRYRAQHTGILKIVAOM	136	
Db	97	TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLIIISDRPLSVTRAVSRAQOQNTTRVRKM	156	
Qy	137	VAVMILAFVNGPMILASDSWK-----NSTNTECECFVTEWYILAITAPLEFLPVS	191	
Db	157	LLVWVLAFLYGPAIL---SWEYLSGSGSIPEGHCAEFYFNWYFLITASTLEPFPFLS	213	
Qy	192	VTFPSVOIY-----WSLWRGSLSRCPSH	215	
Db	214	VTFPNLSIYLNIOQRTRLRDGAEGGPEPPPEAQPSPPPPGCGWCKQGHGEAMPLH	273	
Qy	216	-----AGFIATSSRGTHSRRTGLACRTSLPGLKEPAASLHSSSPRGSLLV	263	
Db	274	RYGVGEAAGAEAGETALGGGGGG-----AASPTSSG-----SSSRGTERPR-----	318	

QY 264 SLRTHMSGIIAFKVGSCFSESPVLHOR-----EHVELLRGRKLARSIAVLISAF 314
Db 319 -----SLKRGSKPASASLEKRMKWSQSFTQRFRLSRDRKVAKSLAVISIF 367
QY 315 AICWAPYCLFTIVLSTYRGERPKSIWYSIAFLQWNSLINPFLYPLCHRRKQKAFWKI 374
Db 368 GLCWAPYTLMIIRAAC-HGHCVPDYWYETSFLLMANSVAVNPVLYPLCHHSFRRAFTKL 426
QY 375 LCVTK-----QPAPSOQ 387
Db 427 LCPQKLIQPHSSLEQ 442
RESULT 2
US-11-115-564-1
; Sequence 1, Application US/11115564
; Publication No. US20050267116A1
; GENERAL INFORMATION:
; APPLICANT: Peschke, Bernd
; APPLICANT: Hohlweg, Rolf
; TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-a]PYRAZINES,
; TITLE OF INVENTION: OCTAHYDROPYRIDO[1,2-a]PYRAZINES AND
; TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-a]AZEPINES
; FILE REFERENCE: 6483.200-US
; CURRENT APPLICATION NUMBER: US/11/115,564
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: US 60/387,047
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-115-564-1
Query Match 33.9%; Score 693; DB 7; Length 445;
Best Local Similarity 37.6%; Pred. No. 1.3e-53;
Matches 163; Conservative 50; Mismatches 124; Indels 96; Gaps 11;
QY 18 LAFMSLAFATIGNAVVILAFVADNRLHRNSNYFPLNLAIISDFPVGVISIPLIYPHTL 77
Db 37 LAALMALLIVATVIGNALVNLAFVADSSLRQTQNNFFLLNLAIISDFLVGAFCIPLIYPVL 96
QY 78 F-NWNPGSIGCMFWLITDYLLCTASVYSIVLISYDRYQSVNAVRYRAQHTGILKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCASSVFNIVLISYDRFLSVTRAVSYRAQQDTRRAVRKM 156
QY 137 VAWVILAFVNGPMILASDVK-----NSTNTECEBPGFVTEWYILAITAFLEFLPVSL 191
Db 157 LLVWVLAFLYLGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 213
QY 192 VVYFSVOIY-----NSLWKRGSLSRCPSH 215
Db 214 VTFNLSIYLNIOQRTRLRDGAREAGPEPPPEAQSPPPPCGCWCKGHEAMPLH 273
QY 216 -----AGFIATSSRGTHSRRTGLACRTSLPGLKEPAASLHSPRGSLLV 263
Db 274 RYGVGEAAGVGEATLGGGGGGS-----VASFTSSG-----SSSRGTERPR----- 318
QY 264 SLRTHMSGIIAFKVGSCFSESPVLHOR-----EHVELLRGRKLARSIAVLISAF 314
Db 319 -----SLKRGSKPASASLEKRMKWSQSFTQRFRLSRDRKVAKSLAVISIF 367
QY 315 AICWAPYCLFTIVLSTYRGERPKSIWYSIAFLQWNSLINPFLYPLCHRRKQKAFWKI 374
Db 368 GLCWAPYTLMIIRAAC-HGHCVPDYWYETSFLLMANSVAVNPVLYPLCHHSFRRAFTKL 426
QY 375 LCVTK-----QPAPSO 384

Db 427 LCPQKLIQPHSS 439
RESULT 3
US-11-115-564-3
; Sequence 3, Application US/11115564
; Publication No. US20050267116A1
; GENERAL INFORMATION:
; APPLICANT: Peschke, Bernd
; APPLICANT: Hohlweg, Rolf
; TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-a]PYRAZINES,
; TITLE OF INVENTION: OCTAHYDROPYRIDO[1,2-a]PYRAZINES AND
; TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-a]AZEPINES
; FILE REFERENCE: 6483.200-US
; CURRENT APPLICATION NUMBER: US/11/115,564
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: US 60/387,047
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Rat
US-11-115-564-3
Query Match 33.3%; Score 682; DB 7; Length 445;
Best Local Similarity 37.0%; Pred. No. 1.2e-52;
Matches 160; Conservative 51; Mismatches 133; Indels 88; Gaps 10;
QY 18 LAFMSLAFATIGNAVVILAFVADNRLHRNSNYFPLNLAIISDFPVGVISIPLIYPHTL 77
Db 37 LAALMALLIVATVIGNALVNLAFVADSSLRQTQNNFFLLNLAIISDFLVGAFCIPLIYPVL 96
QY 78 F-NWNPGSIGCMFWLITDYLLCTASVYSIVLISYDRYQSVNAVRYRAQHTGILKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCASSVFNIVLISYDRFLSVTRAVSYRAQQDTRRAVRKM 156
QY 137 VAWVILAFVNGPMILASDVK-----NSTNTECEBPGFVTEWYILAITAFLEFLPVSL 191
Db 157 ALVWVLAFLYLGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 213
QY 192 VVYFSVOIY-----NSLWKRGSLSRCPSH 215
Db 214 VTFNLSIYLNIOQRTRLRDGAREAGPEPPPEAQSPPPPCGCWCKGHEAMPLH 273
QY 216 AGFIATSSRGTHSRRTGLACRTSLPGLKEPAASLHSPRGSLLVSLRT 267
Db 274 RYGVGEAGPQVEAGEAALGGSGGGAASPTSSG-----SSSRGTERPR----- 318
QY 268 HMSGSIIAFKVGSFCRSESPVLHOR-----EHVELLRGRKLARSIAVLISAFICW 318
Db 319 -----SLKRGSKPASASLEKRMKWSQSFTQRFRLSRDRKVAKSLAVISIFGLCW 371
QY 319 APYCLFTIVLSTYRGERPKSIWYSIAFLQWNSLINPFLYPLCHRRKQKAFWKILCVT 378
Db 372 APYTLMIIRAAC-HGRCIPDYWYETSFLLMANSVAVNPVLYPLCHYSFRRAFTKLCPQ 430
QY 379 K---QPAPSOQ 387
Db 431 KLKVQPHGSLEQ 442

RESULT 4
US-11-241-956-3
; Sequence 3, Application US/11241956
; Publication No. US20060024792A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS INC.; BAUGHN, Mariah R.;
; APPLICANT: GRAUL Richard C.; CHAWLA, Narinder K.;
; APPLICANT: GANDHI, Ameena R.; HAFALIA, April J.A.;


```

; APPLICANT: RAMKUMAR, Javalaxmi; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael B.; KALLICK, Deborah A.;
; APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;
; APPLICANT: BURFORD, Neil; KHAN, Farrah A.;
; APPLICANT: YUE, Henry; LU, Yan;
; APPLICANT: ARVIZU, Chandra S.; ROOPA, Reddy M.;
; APPLICANT: NGUYEN, Denniel B.; LEE, Ernestine A.;
; APPLICANT: LU, Dyung Aina M.; ISON, Craig H.;
; APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0236 USN
; CURRENT APPLICATION NUMBER: US/11/241,956
; CURRENT FILING DATE: 2005-10-04
; PRIOR APPLICATION NUMBER: US/10/398,036
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: PCT/US01/30661
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/245,855
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/242,322
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/240,589
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/249,343
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/247,587
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/245,900
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/242,223
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/236,546
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; FEATURE:
; OTHER INFORMATION: Incyte ID No: 7474823CD1
US-11-241-956-3

Query Match
Best Local Similarity 29.0%; Score 594; DB 7; Length 441;
Matches 115; Conservative 17; Mismatches 29; Indels 10; Gaps 3;

Qy 47 RHRSNYFFLN----LAISDF-----VGVISIPLYIPHTLFWNPGSGICMFWMLTIDYLLC 98
Db 92 RERTNLVLMKKWEFLFVDPDTFVVTQQSVISIPLYIPHTLFEWDFGKEICVFWMLTIDYLLC 151
Qy 99 TASVYSIVLSYDRYQSVSNVAVRAOHTGILKIVAOVAVTILAFVNGPMLIASDSWK 158
Db 152 TASVYNIVLSYDRYLSVSNVAVRYTQHTGVLKIVLVAWVLAFLVNGPMLIVSESWK 211
Qy 159 NSTNTERCEPGFTWETYLAITAPLEFLPVSLVVVFSVOIYWSLWKRGSL 209
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RESULT 5
US-11-124-368A-183
; Sequence 183, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CU001524
; CURRENT APPLICATION NUMBER: US/11/124,368A

; APPLICANT: MERCHERS, Pascal G.
; APPLICANT: Spittaels, Koenraad P. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27, 800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/503,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590

; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-183

Query Match
Best Local Similarity 19.7%; Score 403.5; DB 7; Length 590;
Matches 131; Conservative 85; Mismatches 163; Indels 161; Gaps 19;

Qy 2 SESNGTDVLPPLTAQ-----VPLAFLMSLAFATIGNAVVILAFVADRLNLRHSNYPFLN 56
Db 50 SSPDGTDDPLGGHTVQVVFIAFLTGILAVTIIGNILVIVSPKYNKQLKTVNNYFLLS 109
Qy 57 LAISDFPVGVISIPLYIPHTLFWNPGSGICMFWMLTIDYLLCTASVYSIVLSYDRYQSV 115
Db 110 LACADLIIGVISMNLFTTYIMRWALGNLACDLWLDAIDYVASNASVMNLLVISFDRYFS 169
Qy 116 VSNVAVRYRAOHTGILKIVAOVAV--WILAFVNGPMLIASDSW-----KNSTNTERCEPG 169
Db 170 ITRPLTYRAKRT--TKRAGVMIGLAWVIFVLWAPAIL---FWQYFVGKRTVPFGBCFIQ 224
Qy 170 FVTEWILAITAPLEFLPVSLVVVFSVOIYWSLWK-----HAGF-----218
Db 281 VHPGTSSRSCSSVYELQQSMKRSNRKRGCRHPWFTTKSWKPSSEQMDQDSSSDSWNNN 340
Qy 219 -IATSRGTGHSRRTGLACRT-----SLPG-----242
Db 341 DAAASLENSASSDEEDIGSETRAIYSIVLKLPGHSTILNSTKLPSDNLQVPEELGMVD 400
Qy 243 LKEPAASLHSES-----PRGKSSLLVSLR-----THMSGI-----IAPKV 278
Db 401 LERKADKLAQKSVDDGGSPKSPKLPQLQESAVDTAKTSDVNSVSGKSTALPLSFKE 460
Qy 279 GS-----FCHSESPVLHOREHVELLRGRKLARSIAVLLSAFAICWAPYCLFTVILSVYRG 334
Db 461 ATLAKEFALKTRSQITKRKMSLVKEKAAQTLAAILAFIITWTPTVNMVLV-NTFCDS 519
Qy 335 ERPKSITWYSIAFWLQWNSLINPFLYPLCHRRPQKAPFKIL----CVTKQAPSPQTSQSVSS 391
Db 520 CIPKFTW-NLGYWLCYINSTVNPVVCYALCNKTRFTTFRKMLLLCQCCKKRRKKQYQORQS 578

RESULT 6
US-11-127-877-54
; Sequence 54, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad P. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27, 800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/503,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
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Db 134 SITQAIENLKRTP-RRIKAIITVWVISAVISFPPLISIEKKGGGQPOAEPRCEIND 192
Qy 172 TEWYILAITAFLEFLPVSLVYVFSYQIYWSLWKGSLRCPSHAGFIATSSRGTHSRR 231
Db 193 QKWYVIS-SCIGSFFAPCLMILVYVRIYQIAKRTRVP--PSRRGPDVAAPPGGTERR 249
Qy 232 -TGLAC-RTSLPG-----LKEPAAASHSE----- 253
Db 250 PKGLGPERSAGFGAEPLPTQLNGAPGEPAPAGPRDTDALDLESSSDHAERPPGPR 309
Qy 254 -----SPRGKSSLVS-----LRTHMSGSIIAFKVGSFCRSESPVLHOR 292
Db 310 RPERGPRGKGKARASQVKPGDSLPRRPGCATGIGTPAAGP-GEERVCAAKASRWGRQNR 368
Qy 293 EHVELLRGRKLARSLAVLLSAFAICHAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWEN 352
Db 369 E-----KRFTFLAVVIGVFVVCWPPF-FFTTLTAVGCSV-PTL-FKFFFWFGYCN 418
Qy 353 SLINPLYPLCHRRFOKAFWKILC 376
Db 419 SSLNPVIYTI FNHDFRAFKILC 442
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Search completed: April 26, 2006, 21:01:43
Job time : 27 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2006, 01:31:43 ; Search time 249 Seconds
(without alignments)
2791.272 Million cell updates/sec

Title: US-10-626-126-9

Perfect score: 2045

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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1403.5	68.6	1173	3	US-09-812-216-1
3	1403.5	68.6	1173	3	US-09-875-076-13
4	693	33.9	1335	2	US-08-985-090-3
5	693	33.9	1335	3	US-09-165-543-3
6	693	33.9	1335	3	US-09-167-354-6
7	693	33.9	1335	3	US-09-642-855-6
8	693	33.9	1335	3	US-09-642-514-6
9	693	33.9	1335	3	US-09-642-852-6

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20	682	33.3	1338	3	US-09-165-543-6
21	682	33.3	1953	3	US-09-891-053-26
22	682	33.3	3244	3	US-09-165-543-4
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ALIGNMENTS

RESULT 1

US-09-414-010-1
; Sequence 1, Application US/09414010

; Patent No. 6204017

; GENERAL INFORMATION:

; APPLICANT: Behan, Jiang Xu

; APPLICANT: Hedrick, Joseph A.

; APPLICANT: Laz, Thomas M.

; APPLICANT: Monsma, Frederick J. Jr.

; APPLICANT: Morse, Kelley L.

; APPLICANT: Umland, Shelby P.

; APPLICANT: Wang, Suke

; TITLE OF INVENTION: Histamine receptor

; FILE REFERENCE: CN01069

; CURRENT APPLICATION NUMBER: US/09/414,010

; CURRENT FILING DATE: 1999-10-07

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-414-010-1

Alignment Scores:			
Pred. No.:	1.5e-133	Length:	1173
Score:	1403.50	Matches:	271
Percent Similarity:	79.3%	Conservative:	40
Best Local Similarity:	69.1%	Mismatches:	78
Query Match:	68.6%	Indels:	3
DB:	3	Gaps:	2

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Qy	21	LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe	40
Db	61	TTTATGTCTTCTTAGTAGTTTTCGTATATATGCTAGGAAATGCTTTGGTCATTTTATAGCTTTT	120
Qy	41	ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer	60
Db	121	GTGGTGACAAACCCTTAGACATCGAAGTAGTTATTTTCTTAACCTTGGCCATCTCT	180
Qy	61	AspPhePheValGlyValIleSerIlePLeuLeuTyrIleProHisThrLeuPheAsnTyr	80
Db	181	GACTTCTTTGTGGGTGTGATCTCCATCTCCTTTGTATACATCCCTCACAGCTGCTTGGAAATGG	240
Qy	81	AsnProGlySerGlyIleCysMetPheTyrIleuIleThrAspTyrLeuLeuCysThrAla	100
Db	241	GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATATGATACAGCA	300
Qy	101	SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal	120
Db	301	TCTGTATATAACAATGTCTCATCAGCTATGATCATACCTGTGCTCAGTCTCAAATGCTGTG	360
Qy	121	ArgTyrArgAlaGlnHisThrGlyIleLeuIleValIleAlaGlnMetValAlaValTyr	140
Db	361	TCTTATAGAACTCAACATACTCGGGGTCTGTGAAGATTGTTACTCTGATGGTGGCGGTTTGG	420
Qy	141	IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrPheAsnSer	160
Db	421	GTGCTGCCCTTCTTAGTGAATGGGCCAAATGATCTAGTTTCAGAGTCTTGGAGAGTAA	480
Qy	161	ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTyrIleLeuAlaIleThr	180
Db	481	GGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGGTATACATCTTTGCCATCACA	534
Qy	181	AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr	200
Db	535	TCATTTCTTGGAAATTCGTGATCCCACTCATCTTAGTCGCTTATTTTCAACATGAATATTTAT	594
Qy	201	TyrSerLeuTyrPheArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla	220
Db	595	TGGAGCCTGTGAAGCGTGATCATCTCAGTAGGTGCCAAGGCCATCTCGAGCTACACTGCT	654
Qy	221	ThrSerSerArgGlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeu	240
Db	655	GTCTCTTTCCAACATCTGTGGACATCTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT	714
Qy	241	ProGlyLeuIleGluProAlaAlaSerLeuHisSerGluSerProArgGlyLeuSerSer	260
Db	715	TCTGCATCGACAGAAAGTTCTCTGCATCTCTTCATTCAGAGACACAGAGAGAAAGAGTAGT	774
Qy	261	LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer	280
Db	775	CTCATGTTTTCTCAGAACCAAGATGAATAGCAATCAATGCTTCTCCAAATGGGTCC	834
Qy	281	PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly	300
Db	835	TTCTCCCAATCAGATTCTGTAGTCTTTCACCAAGGGAAACATGTTGAATGCTTTAGAGCC	894
Qy	301	ArgLysIleuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTyrAlaPro	320
Db	895	AGGAGATTAGCAAGTCACTGGCCATCTCTTATAGGGGTTTTTGTGTTGCTTGGGCTCCA	954
Qy	321	TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle	340
Db	955	TATTCTCTGTTCACAAATGTCTTTCATTTATTTCTCTCAGCAACAGGTCCTTAATCAGTT	1014
Qy	341	TrpTyrSerIleAlaPheTyrLeuGlnTyrPheAsnSerLeuIleAsnProPheLeuTyr	360
Db	1015	TGGTATAGAAATTTGATTTTGGCTTCAGTGGTTCAATTCCTTTGTCATCTCTTTGTTAT	1074

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Qy 361 ProLeuCysHisIaGargPheGlnLysAlaPheTrpIysIleuCysValThrLysGln 380
Db 1075 CCATTGTGTCCACAGCGCTTTCAAAAGGCTTCTTGAAATATTTTTGTATAAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCATCACACAGTCGGTCAGTATCTTCT 1170

RESULT 2
US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. 6613533
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1

Alignment Scores:
Pred. No.: 1 5e-133 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.3% Conservative: 40
Best Local Similarity: 69.1% Mismatches: 78
Query Match: 68.6% Indels: 3
DB: 3 Gaps: 2

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Db 421 GTGCTGCCCTCTTAGTGAATGGCCCAATGATCTAGTTTCAGAGTCTTGGAGAGTAA 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAAATGGTACATCCTTGCATCACA 534
Qy 181 AlapheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATCTTGGAAATTCGTGATCCCGCATCTCTTAGTCGCTTATTTCACATGAATATTAT 594
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGAAGCTGTGGAAGCGTGATCATCTCAGTAGTGCCAAAGCCATCTCTGACATGCTGCT 654
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAAACATCTGTGCACACTCATCTCAGAGGTAGACTATCTTCAAGGAGATCTCT 714
Qy 241 ProGlyLeuLysGluProAlaIleSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAGTCTCTGCATCTCTTTCATTCAGAGAGACAGAGAGAGAGTAGT 774
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 775 CTATGTCTTCCCAAGAACCAAGATGAATAGCAATACAATGCTTCCAAATGGGTCTC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATCTGTAGCTCTTCACCAAGGGAACATGTGAACCTGCTTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTCTGCTGGCTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTGTGTCAAAATGCTCTTTCATTTATTTCTCAGCAACAGGTCTCTAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1015 TGGTATAGATTCAGATTTGGCTTCAGTGGTTCATTTCTTGTCAATCTCTTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1075 CCATTGTGTCAACAGCGCTTCAAAAGCGTTCTTGAATAATTTTGTATAAAAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTTACCATCACAAACACACACGTGGTCAGTATCTCT 1170

RESULT 3
US-09-875-076-13
; Sequence 13, Application US/09875076
; Patent No. 6869776
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
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; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-076-13

Alignment Scores:
Pred. No.: 1,5e-133 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.3% Conservative: 40
Best Local Similarity: 69.1% Mismatches: 78
Query Match: 68.6% Indels: 3
DB: Gaps: 2

US-10-626-126-9 (1-391) x US-09-875-076-13 (1-1173)
Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACTAATAGCAACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCTTAGTAGCTTTTGTATAATGCTAGGAAATGCTTTGGTCAATTTAGCTTTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAAACCACTTAGACATCGAAGTAGTATTTTTTTCTTAACCTGGCCATCTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTGCAATGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
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301 TCTGTATATAACATTGCTCTCATCAGCTATGATCGATACCTGTCAGTCTCAAAATGCTGTG 360
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuValIleValAlaGlnMetValAlaValTTP 140
Db 361 TCTTATAGAACTCAACATACCTGGGCTCTGAAGATTGTACTCTGATGGTGGCGTTGG 420
QY 141 IleLeuAlaPheLeuValAenGlyProMetIleLeuAlaSerAspSerTrpIlysAenSer 160
Db 421 GTCTGGCCCTCTTAGTGAATGGCCCAATGATTTCTAGTTTCAGAGTCTGGAGAGATGAA 480
QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTCGGAATGGTACATCTCTTGCATCACA 534
QY 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATTTCTGGAATTCGTGATCCAGTCATCTTAGTCGTTATTTCACATGAATATTAT 594
QY 201 TrpSerLeuTrpIlysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCTGTGGAGGTGATCATCTCAGTAGTGGCCAAAGCCATCTCTGGACTGCTGT 654
QY 221 ThrSerSerArgGlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTTT 714
QY 241 ProGlyLeuysGluProAlaAlaSerLeuHisSerGluSerProArgGlyIlysSerSer 260
Db 715 TCTGCATCGACAAGTTCCTGCATCTCTTTCATTCAGAGAGACAGAGGAGAAAGTAGT 774
QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleAlaPheIlysValGlySer 280
Db 775 CTATGTTTCTTCAAGAACCAAGATGAATAGCAATCAATTCCTTCCAAATGGGTTC 834
QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATCTGTAGCTCTTCAACAAAGGGAACATGTTGAATCTGTAGGCC 894
QY 301 ArgIysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCCAAAGTCACTGGGCCATTCCTTAGGGGTTTTCCTGTCTGGTGGCTCCA 954
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProIlysSerIle 340
Db 955 TATCTCTGTTCACATTTGCTTTCATTTATTCCTCAGCAACAGTCTCTAATCAGTT 1014
QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAenProPheLeuTyr 360
Db 1015 TGGTATAGAATTGCAATTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCTCTTTGTAT 1074
QY 361 ProLeuCysHisArgArgPheGlnIysAlaPheTrpIlysIleLeuCysValThrIysGln 380
Db 1075 CCATTGTGTACAAAGCGCTTCAAAAGGCTTCTTGAATAATATTTGTATATAAAAGCAA 1134
QY 381 ProAlaProSerGln--ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCACACACAGCTCGGTGATATCTTCT 1170

RESULT 4

US-08-985-090-3
; Sequence 3, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090

FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jean M. Silveri

REGISTRATION NUMBER: 39,030

REFERENCE/DOCKET NUMBER: MNI-032

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1335 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1335

US-08-985-090-3

Alignment Scores:

Pred. No.: 8,2e-61 Length: 1335
Score: 693.00 Matches: 163
Percent Similarity: 49.2% Conservative: 50
Best Local Similarity: 37.6% Mismatches: 124
Query Match: 33.9% Indels: 96
DB: 2 Gaps: 11

US-10-626-126-9 (1-391) x US-08-985-090-3 (1-1335)

QY 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValAlaIle 37
Db 109 CTGGCGCGCTCATGGCGTGTCTCATCGTGGCGCACGCGTGTGGCGTGTGGTGTG 168
QY 38 LeuAlaPheValAlaAspArgAenLeuArgHisArgSerAsnTyrPhePheLeuAenLeu 57
Db 169 CTGCGCTTCTGTGGCGGACTCGAGCCTCCGACCCAGAACAACTTCTTCTGCTCAACCTC 228
QY 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
Db 229 GCATCTCCGACTTCTCTCGGGCGCTTCTGCATCCCATCTGATGATACCTACGTGCTG 288
QY 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 289 ACAGCGCGCTGGACCTTCGCGCGGGCGCTCTGCAAGCTGTGGCTGTAGTGGACTACCTG 348
QY 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 349 CTGTGCACCTCTCTCTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGTGGTCCG 408
QY 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuIlysIleValAlaGlnMet 136
Db 409 ACCGAGCGGTCTCATACCGGCGCCAGAGGGTGACACGCGGGCGGCGAGTCCGGAAGATG 468
QY 137 ValAlaValTrpIleLeuAlaPheLeuValAenGlyProMetIleLeuAlaSerAspSer 156
Db 469 CTGCTGTGTGGTGTGGCTTCTCTGCTGTACGACACCGACCATCTCTG-----AGC 519
QY 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 520 TGGAGTACTGTTCGGGGGCGAGCTCCATCCCGAGGGCCACTGCTATGCCGAGTTCTTC 579
QY 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuLeuProValSerLeu 191

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Db 580 TAACTGGTACTTCCATCACGGCTTCCACCGCTGGAGTTCTTTACGCCCTTCTCAGC 639
Qy 192 ValValTrpPheSerValGlnIleTyr-
Db 640 GTACACTTCTTAACTCAGCATCTACTGAACATCCAGAGCGCACCGCTCGGCTG 699
Qy 200 -----
Db 700 GATGGGCTCGAGAGCGAGCGCGCCGAGCCCTCCGAGCGCCAGCCCTCACACCC 759
Qy 201 -----
Db 760 CCACCGCTGGCTCTGGCGCTGTGGAGAGGCGGACGGGAGGCGATGCCCTGCAC 819
Qy 216 -----
Db 820 AGGTATGGGTGGGTGAGCGCGGTAGCGCTGAGCGCGGAGCGGACCTCGGGGT 879
Qy 224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
Db 880 GCGGTGGGGCGGCTCC-----GTGGCTTCAACCCACCTCCAGCTCCGGC--- 924
Qy 244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuVal 263
Db 925 -----
Qy 264 SerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySerPheCysArg 283
Db 955 -----
Qy 284 SerGluSerProValLeuHisGlnArg-----
Db 982 GCGTCTCGGCTCACTGGAGAGCGCATGAAGATGGTGTCCAGAGCTTCCACCGCGC 1041
Qy 295 ValGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuSerAlaPhe 314
Db 1042 TTTGGGCTGTCTCGGACAGAAAGTGGCTGTGGCGGTTCATCGTGAGCATCTTT 1101
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgGly 334
Db 1102 GGGCTGTGTGGGCCCCATACACCTCTCTGTATCATCCGGCGCGCTGC---CATGGC 1158
Qy 335 GluArgProLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
Db 1159 CACTGCTGCTGACTACTGTGTACAAACCTCTCTGTGCTGTCTGTGGGCAACTCGCT 1218
Qy 355 IleAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysVal 374
Db 1219 GTCAACCTGTCTCTACCTCTGTGTGCACACAGCTTCCGCGGGCTTCCACCAAGCTG 1278
Qy 375 LeuCysValThrLys-----GlnProAlaProSer 384
Db 1279 CTCTGCCCCAGAGCTCAAAATCCAGCCCCACAGCTCC 1317
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RESULT 5

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US-09-165-543-3
; Sequence 3, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
; US-09-165-543-3
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Alignment Scores:
Pred. No.: 8-2e-61 Length: 1335
Score: 693.00 Matches: 163
Percent Similarity: 49.2% Conservative: 50
Best Local Similarity: 37.6% Mismatches: 124
Query Match: 33.9% Indels: 96
DB: 3 Gaps: 11
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US-10-626-126-9 (1-391) x US-09-165-543-3 (1-1335)

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Qy 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValle 37
Db 109 CTGGCGCGCTCATGGCGTCTCATGTGCCACGGTGTGGCAACAGCGCTGTCATG 168
Qy 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPheLeuAsnLeu 57
Db 169 CTCGCTCTGTGGCGGACTCGAGCTCCGACCCAGAACAACTCTTCTCTGCTCAACCTC 228
Qy 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
Db 229 GCCATCTCCGACTCTCTGCTGGGGCTTCTGTATCCCATCTATGTATGATACCTAGTGTG 288
Qy 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 289 ACAGGCGCTGGACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGAGTACTACTG 348
Qy 97 LeuCysThrAlaSerValTyrSerIleValIleSerTyrAspArgTyrGlnSerVal 116
Db 349 CTGTGCACCTCTCTGCTTCAACATGCTGCTCATCAGCTACGACCGCTTCTCTGCTCGGTC 408
Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMet 136
Db 409 ACCGAGCGGTCTCATACCGGGCCAGAGGTGACACGGCGGGGAGTGTGGGAAGATG 468
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 469 CTGCTGTGTGGTGTGCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 519
Qy 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 520 TGGAGGTACCTGTTCGGGGGCGAGCTCCATCCCGAGGGCCAGCTGCTATGCGAGTTCTTC 579
Qy 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
Db 580 TACAACCTGGTACTCTCTCATCAGGCTTCCACCGCTGGAGTTCTTTACGCCCTTCTCTCAGC 639
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QY 192 ValValTyrPheSerValGlnIleTyr----- 200
DB 640 GTACACTTCTTTAACTCAGCATCTACCTGAACATCCAGAGGCGCACCCCGCTCCGGCTG 699

QY 200 ----- 200
DB 700 GATGGGGCTCGAGAGGCGAGCCGCCCGAGCCCTCCCGAGGCCCGCCCTCACCACCC 759
QY 201 -----TrpSerLeuTyrPheLysArgGlySerLeuSerArgCysProSerHis 215
DB 760 CCACCGCTGGCTGCTGGGCTCTGCGAGAGGGGCGACGGGAGGCCATGCGCGCTGCAC 819

QY 216 -----AlaGlyPheIleAlaThrSerSer 223
DB 820 AGTATGGGGTGGGTAGGGCGCGGTAGGGCTGAGCGCGGGAGGGGACCTCCGGGGT 879

QY 224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
DB 880 GCGGGTGGGGCGGCTCC-----GTGGCTTCAACCTCCAGCTCCAGCTCCGGC--- 924

QY 244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuLeuVal 263
DB 925 -----AGCTCTCGAGGGGCACTGAGAGGCGCGC----- 954

QY 264 SerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySerPheCysArg 283
DB 955 -----TCACTCAAGAGGGGCTCCAAGCGCTCG 981

QY 284 SerGluSerProValLeuHisGlnArg-----GluHis 294
DB 982 GCGTCTCGGCTCACTGGAGAGCGCATGATGGTGTCACAGCTTCAACCCAGCGC 1041

QY 295 ValGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPhe 314
DB 1042 TTTTGGGTGTCTCGGACAGAAAGTGGCCAGTGTGCGCTCATCGTGAGCATCTT 1101

QY 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
DB 1102 GGGCTGTGTGGGCCCCATACAGCTGTCTGATGATATCCGGGCGCGCTCG---CATGGC 1158

QY 335 GluArgProLysSerIleTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
DB 1159 CACTGGCTCCCTGACTACTGTGTAGAAACCTCTTCTGGCTCTGTGGGCCAACTCGGCT 1218

QY 355 IleAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
DB 1219 GTCAAGCTGTCTCTACCTCTGTGCGCACACAGCTTTCGCGGGGCTTCAACAAGCTG 1278

QY 375 LeuCysValThrLys-----GlnProAlaProSer 384
DB 1279 CTCTGCCCCCAGAAGCTCAAAATCCAGCCCCACAGCTCC 1317
```

RESULT 6

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US-09-167-354-6
; Sequence 6' Application US/09167354A
; Patent No. 613559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
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/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-167-354-6
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Alignment Scores:
Pred. No.: 8,2e-61 Length: 1335
Score: 693.00 Matches: 163
Percent Similarity: 49.2% Conservative: 50
Best Local Similarity: 37.6% Mismatches: 124
Query Match: 33.9% Indels: 96
DB: Gaps: 11
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US-10-626-126-9 (1-391) x US-09-167-354-6 (1-1335)

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QY 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIle 37
DB 109 CTGGCGCGCTCATGGCGCTGTCTCATCTGTGGCCACCGTGTGGCAACGGCTGGTCATG 168

QY 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
DB 169 CTGGCTTCTGTGGCGACTCGAGCTTCGACCCACAGACAACTTCTTCTGTCTCAACCTC 228

QY 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
DB 229 GCCATCTCGGACTTCTCTGTGGCGCTTCTGTGCATCCCATGTATGTACCTACGTGCTG 288

QY 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
DB 289 ACAGGCGCTGACCTTCGCGCGGCTCTGTCAAGCTGTGGCTGTGTAGTGGACTACCTG 348

QY 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
DB 349 CTGTGCACCTCTCTGCTTCAACATCGTGTCTCATCAGCTACGACGCTTCTGTGCGTC 408

QY 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMet 136
DB 409 ACCCGAGCGGTCTCATACCGGCGCCACAGGGGTGACACGCGGCGGCGAGTGCAGAGATG 468

QY 137 ValAlaValTyrIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
DB 469 CTGTGTGTGGTGTGGCTTCTGTCTGTGTACGGACCAAGCATCCTG-----AGC 519

QY 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
DB 520 TGGAGTACTGTTCGGGGGCGAGCTCCATCCCGAGGCGCACTGTCTATGCGAGTCTTCTC 579

QY 172 ThrGluTyrTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuLeuProValSerLeu 191
DB 580 TACAACCTGGTACTTCTCATACGGCTTCCACCTGGAGTCTTTTACGCCCTTCTCTCAGC 639

QY 192 ValValTyrPheSerValGlnIleTyr----- 200
DB 640 GTACACTTCTTTAACTCAGCATCTACCTGAACATCCAGAGGCGCACCCCGCTCCGGCTG 699

QY 200 ----- 200
DB 700 GATGGGGCTCGAGAGGCGAGCCGCCCGAGCCCTCCCGAGGCCCGCCCTCACCACCC 759

QY 201 -----TrpSerLeuTyrPheLysArgGlySerLeuSerArgCysProSerHis 215
DB 760 CCACCGCTGGCTGCTGGGCTGTGCGAGAGGGGCGACGGGAGGCCATGCGCGCTGCAC 819

QY 216 -----AlaGlyPheIleAlaThrSerSer 223
DB 820 AGTATGGGGTGGGTAGGGCGCGGTAGGGCTGAGCGCGGGAGGGGACCTCCGGGGT 879

QY 224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
DB 880 GCGGGTGGGGCGGCTCC-----GTGGCTTCAACCTCCAGCTCCAGCTCCGGC--- 924

QY 244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuLeuVal 263
DB 925 -----AGCTCTCGAGGGGCACTGAGAGGCGCGC----- 954
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Qy 264 SerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySerPheCysArg 283
Db 955 ---TCACCAAGAGGGGCTCCAAAGCCGTCG 981
Qy 284 SerGluSerProValLeuHisGlnArg--- 294
Db 982 GCGTCCTCGGCTCGTGGAGAGCGCATGAGATGCTGCCAGAGCTTCACCCAGCGC 1041
Qy 295 ValGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPhe 314
Db 1042 TTTCCGGCTGTCTCGGACAGGAAAGTGCCAAAGTCGCTGCGCTCATCGTAGCATCTTT 1101
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
Db 1102 GGGCTGTGCTGGGCCCCATACACGCTGCTGATGATCATCCGGGCGCGCTGC---CATGGC 1158
Qy 335 GluArgProLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
Db 1159 CACTGGCTCCCTGACTACTGGTAGCAAAACCTCTCTTCTGGCTCTGTGGGCCAACTCGGCT 1218
Qy 355 IleAsnProPheLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIle 374
Db 1219 GTCAACCTGTGCTCTACCTCTGTGCGCACACAGCTTTCGCGGGCTTTCACCAAGCTG 1278
Qy 375 LeuCysValThrLys-----GlnProAlaProSer 384
Db 1279 CTCTGCCCCCAGAGCTCAAAATCCAGCCCCACAGCTCC 1317
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RESULT 7

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US-642-855-6
; Sequence 6, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; PRIOR FILING DATE: 2000-08-21
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-6
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Alignment Scores:
Pred. No.: 8.2e-61 Length: 1335
Score: 693.00 Matches: 1335
Percent Similarity: 49.2% Conservative: 50
Best Local Similarity: 37.6% Mismatches: 124
Query Match: 33.9% Indels: 96
DB: 3 Gaps: 11
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US-10-626-126-9 (1-391) x US-09-642-855-6 (1-1335)

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Qy 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIle 37
Db 109 CTGGCCCGCTCATGGCGCTGCTCATCGTGCCACGCTGGGCAACGCGCTGTCATG 168
Qy 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 169 CTGCGCTCTGTGGCCGAGCTCGAGCTCCGCCACCAAGAACTTCTTCTGCTCNACCTC 228
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Qy 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
Db 229 GCCATCTCCGACTCTCTGCTCGCGGCTTCTGCATCCACTGATGTATACCTAGCTGCTG 288
Qy 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 289 ACAGGCGCTGGACCTTGGCGCGGGCTCTGCAAGCTGTGGCTGTAGTAGTACTACCTG 348
Qy 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 349 CTGTGACACCTCTCTGCTTCAACATCGTGTCTCATGCTACACCGCTTCTGTCGGTGC 408
Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMet 136
Db 409 ACCGAGCGGTCTCATACCGGCGCCAGCGGGTGACACGCGGGCGGCGAGTGCAGAGATG 468
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 469 CTGCTGTGTGGGTGTGGCTTCTCTGCTGTACGGACCAAGCCATCTCTG---AGC 519
Qy 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 520 TGGGAGTACCTGTCTCGGGGCGAGCTCCATCCCGAGGGCCACTGCTATGCCGAGTTCTTC 579
Qy 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
Db 580 TACAACCTGTGTACTCTCTCATCAGGGCTTTCACCTGTGAGTTCCTTACGCCCTTCTCTCAGC 639
Qy 192 ValValTyrPheSerValGlnIleTyr----- 200
Db 640 GTCACTCTCTTTAACTCAGCATCTACCTGAACATCCAGAGGCGCACCCGCTCCGGCTG 699
Qy 200 ----- 200
Db 700 GATGGGGCTCGAGAGGCGAGCGCGCCCGAGCCCTCCCGAGGCCAGCCCTCACCACCC 759
Qy 201 -----TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHis 215
Db 760 CCACCGCTGTGTGTGGGCTCTGTGCGAGAGGCGACGCGGAGGCGCATGCCCTGCAC 819
Qy 216 -----AlaGlyPheIleAlaThrSerSer 223
Db 820 AGGTATGGGGTGGGTGAGCGCGCGTAGGCGCTGAGGCGCGGAGGCGACCTCCGGGGT 879
Qy 224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
Db 880 GCGGTGGGGCGGCTCC-----GTGGCTTCAACCCACCTCCAGCTCCGCGC--- 924
Qy 244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuVal 263
Db 925 -----AGCTCTCGAGGGGCACTGAGAGGCGCGC----- 954
Qy 264 SerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySerPheCysArg 283
Db 955 -----TCACCAAGAGGGGCTCCAAAGCCGTCG 981
Qy 284 SerGluSerProValLeuHisGlnArg-----GluHis 294
Db 982 GCGTCTCGGCTCGCTGGAGAGCGCATGAGATGCTGCCAGAGCTTTCACCCAGCGC 1041
Qy 295 ValGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPhe 314
Db 1042 TTTCCGGCTGTCTCGGACAGGAAAGTGCGCTGCTGGCGCTCATCGTAGCATCTTT 1101
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
Db 1102 GGGCTGTGCTGGGCCCCATACACGCTGCTGATGATCATCCGGGCGCGCTGC---CATGGC 1158
Qy 335 GluArgProLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
Db 1159 CACTGGCTCCCTGACTACTGGTAGCAAAACCTCTCTTCTGCTCTGTGGGCGCAACTCGGCT 1218
Qy 355 IleAsnProPheLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIle 374
```



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; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-852-6

Alignment Scores:
Pred. No.:      8.2e-61      Length:      1335
Score:          693.00      Matches:      163
Percent Similarity: 49.3%      Conservative: 50
Best Local Similarity: 37.6%      Mismatches: 124
Query Match:      33.9%      Indels:      96
DB:              3          Gaps:      11

US-10-626-126-9 (1-391) x US-09-642-852-6 (1-1335)

Qy 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIle 37
Db 109 CTGGCCGCGCTCATGGCGCTGCTCATGTGGCCACGGTGTGGCAACGGCGTGTGTCATG 168
Qy 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 169 CTCGCCCTTCGTGGCGGAGCTCGAGCCTCGCACCCAGAACCAACTTCTTCTGCTCAACCTC 228
Qy 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
Db 229 GCCATCTCCGACTTCTCGTGGCGGCTTCTGCACTCCACCTGATGATGACCTACGTGCTG 288
Qy 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 289 ACAGCGCGCTGGACCTTCGGCGCGGCTCTGCAAGCTGTGGCTGTGTAGTGACTACCTG 348
Qy 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 349 CTGTGCACCTCTCTGCTGCTCAACATGCTGCTCATAGCTACGACCGCTTCTGCTGCGTC 408
Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMet 136
Db 409 ACCGAGCGGTCTCATACCGGCGCCAGAGGTGACAGCGGGCGGCGAGTGGCGGAAGATG 468
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 469 CTGCTGTGTGGGTGCTGGCTTCTCTGTGTACGACCGACCCATCTCTG-----AGC 519
Qy 157 TrpIys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 520 TGGGAGTACCTGTCCGGGGGCGAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTCTTC 579
Qy 172 ThrGluTrpTrpIleLeuAlaIleThrAlaPheLeuGluPheLeuLeuProValSerLeu 191
Db 580 TACAACTGGTACTTCTCATCAGCGCTTCCACCGCTGGAGTTCTTTACGCGCTTCTCTCAGC 639
Qy 192 ValValTyrPheSerValGlnIleTyr----- 200
Db 640 GTACCTTCTTAACTTCAGCACTACTCTGACATCCAGAGGGCGACCGCGCTCGGCTG 699
Qy 200 ----- 200
Db 700 GATGGGCTCGAGAGGCGCGCGCCCGAGCCCTCCCGAGGGCCAGCCCTCACACCC 759
Qy 201 -----TrpSerLeuTrpIysArgGlySerLeuSerArgCysProSerHis 215
Db 760 CCACCGCTGCTGCTGGGGTGTGTGCGAGAGGGGCGACGGGGGCGCATGCCGCTGCAC 819
Qy 216 -----AlaGlyPheIleAlaThrSerSer 223
Db 820 AGGTATGGGTGGGTGAGGGCGCGGTAGGGCGCTGAGGCGCGGGAGGGCGACCTCGGGGGT 879
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224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
880 GCGCGTGGGGCGGCTCC-----:GTCCTTCAACCCACTCCAGCTCCGCGC--- 924
244 LysGluProAlaAsrLeuHisSerGluSerProArgGlyIysSerSerLeuVal 263
925 -----AGCTCTCGAGGGGCACTGAGAGGGCGCGC----- 954
264 SerLeuArgThrHisMetSerGlySerIleAlaPheIysValGlySerPheCysArg 283
955 -----TCACTCAAGAGGGGCTCCAAGCCGCTCG 981
284 SerGluSerProValLeuHisGlnArg-----GluHis 294
982 GCGTCTCGCGCTCGCTGGAGAGCGCATGAAGATGTGTGCCAGAGCTTCACCCAGCGC 1041
295 ValGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuSerAlaPhe 314
1042 TTTCCGGCTGTCTCGGACAGGAAAGTGCCTGCTGCGCTCATCGTGAGCATCTTT 1101
315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
1102 GGGCTCTGCTGGGCGCCCATACAGCTGCTGATGATCATCCGGCGCGCTGC---CATGGC 1158
335 GluArgProIysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
1159 CACTGCGTCCCTGACTACTGTACGAAACCTCTCTTGGCTCTGTGGCGCACTCGGCT 1218
355 IleAsnProPheLeuTyrProLeuCysHisArgPheGlnIysAlaPheTrpLysIle 374
1219 GTCAACCTGTCTCTACCTCTGTGGCACCACAGCTTCGCGGGGCTTCACCAAGCTG 1278
375 LeuCysValThrIys-----GlnProAlaProSer 384
1279 CTCTGCCCCAGAGCTCAAAATCCAGCCCCACAGCTCC 1317

RESULT 10
US-09-891-053-21
; Sequence 21, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 2050
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (271) ... (1629)
US-09-891-053-21

Alignment Scores:      1.66e-60      Length:      2050
Pred. No.:              693.00      Matches:      163
Score:
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Percent Similarity: 49.2%      Conservative: 50
Best Local Similarity: 37.6%    Mismatches: 124
Query Match: 33.9%             Indels: 96
DB: 3                           Gaps: 11

US-10-626-126-9 (1-391) x US-09-891-053-21 (1-2050)

QY 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAenAlaValIle 37
DB CTGGCGCGCTCATGGCGTCTCATCGTGCACCGGTGTGGGCAAGCGCTGCATG 438
QY 38 LeuAlaPheValAlaAsePArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAenLeu 57
DB CTGGCGCTTCGTGGCGGACTCGAGCTCCGACCCAGAACAACTTCTTCCTGTCTCAACCTC 498
QY 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
DB GCCATCTCCGACTTCTCGTGGCGCTTCGTATCCCACTGTATGATACCTACGCTGCTG 558
QY 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
DB ACAGCGCGCTGGACCTTCGGCGGGGCTCTGCAAGCTGTGGTGTGGTGTGGTGTGGTGTG 618
QY 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
DB CTGTGCACCTCTCTGCTTCAACATCGTCTCATCAGCTACGACCGCTTCCTGTGGTGC 678
QY 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMet 136
DB ACCCGAGCGGTCTCATACCGGGGCCAGCAGGGTGACACGCGGGCGGCGGTGCGGAGATG 738
QY 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
DB CTGCTGTGTGGTGTGGCTTCTGCTGTACGACCAAGCCATCTCTG-----AGC 789
QY 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
DB TGGAGTGTACCTGTCCGGGGGCGAGCTCCATCCCGAGGGCCACTGCTATGCGCGATTCTTC 849
QY 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
DB TACAACCTGGTACTTCTTCATCAGCGCTTCCACCTTGGAGTTCTTTAGCGCCCTTCTCAGC 909
QY 192 ValValTyrPheSerValGlnIleTyr----- 200
DB GTACCTTCTTTAACCTACGACTACTGAAATCCAGAGGCGCACCCCGCTCCGGCTG 969
QY 200 ----- 200
DB GATGGGCTCGAGAGGCGAGCGCGCGCGCCCTCCCGAGGCCCGAGCCCTCACCACCC 1029
QY 201 -----TrpSerLeuTyrPheArgGlySerLeuSerArgCysProSerHis 215
DB ----- 1030
DB CCACCGCTGGCTGTGGGCTGTGTGCAGAGGGGCGAGGAGGCGCATGCGCGTGCAC 1089
QY 216 -----AlaGlyPheIleAlaThrSerSer 223
DB AGGTATGGGTGGTGTGGCGCGGTAGGCGCTGAGCGCGGGGAGGGGACCCCTCGGGGT 1149
QY 224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
DB GGCGGTGGGGCGGCTCC-----GTGGCTTCAACCCACTCCAGCTCCGCGC--- 1194
QY 244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuLeuVal 263
DB -----AGCTCTCGAGGGGCACTGAGAGGCGCGCGC----- 1224
QY 264 SerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySerPheCysArg 283
DB -----TCACTCAAGAGGGGCTCCAGCCGCTCG 1251
QY 284 SerGluSerProValLeuHisGlnArg-----GluHis 294
DB -----
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Db 1252 GCGTCTCTCGCGCTCGCTGGAGAAAGCCATGAAGATGGTGTCCAGAGCTTACCCAGCGC 1311
QY 295 ValGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPhe 314
Db 1312 TTTCCGCTGTCTCGGACAGAAAGTGGCAAGTCCGTGGCGCTCATCGTGCATCTTT 1371
QY 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
Db 1372 GGGCTCTGTGGGCGCCCATACACGCTGTGTATGATCATCGGCGCGCTGC---CATGGC 1428
QY 335 GluArgProLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
Db 1429 CACTGGCTCCCTGACTACTGGTACGAAACCTCTCTGGCTCTGTGGGCACTCGGCT 1488
QY 355 IleAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
Db 1489 GTCNACCTGTCTCTACCTCTGTGTCACACAGCTTTCGGCGGGGCTTCACCAAGCTG 1548
QY 375 LeuCysValThrLys-----GlnProAlaProSer 384
Db 1549 CTCTGCCCGCAGAAAGCTCAAAATCCAGCCCGCACAGCTCC 1587

RESULT 11
US-09-949-016-5059
; Sequence 5059, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5059
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5059

Alignment Scores:
Pred. No.: 2,55e-60      Length: 2665
Score: 693.00           Matches: 163
Percent Similarity: 49.2%      Conservative: 50
Best Local Similarity: 37.6%    Mismatches: 124
Query Match: 33.9%          Indels: 96
DB: 3                     Gaps: 11

US-10-626-126-9 (1-391) x US-09-949-016-5059 (1-2665)

QY 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAenAlaValIle 37
Db 400 CTGGCGCGCTCATGGCGTCTCATCGTGCACCGGTGTGGGCAAGCGCTGCATG 459
QY 38 LeuAlaPheValAlaAsePArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAenLeu 57
Db 460 CTGGCGCTTCGTGGCGGACTCGAGCTCCGACCCAGAACAACTTCTTCCTGTCTCAACCTC 519
QY 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
Db 520 GCCATCTCCGACTTCTCGTGGCGCTTCGTATCCCACTGTATGTACCTACGCTGCTG 579
QY 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 580 ACAGCGCGCTGGACCTTCGGCGGGGCTCTGCAAGCTGTGGTGTGGTGTGGTGTGGTGTG 639
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QY 97 LeuCyThrAlaSerValTyrSerIleValIleuSerTyrAspArgTyrGlnSerVal 116
Db 640 CTGTGACCTCTCTCGCTCAACATGCTGCTCATCAGCTACGACCGCTTCCTGTGGTC 699
QY 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMet 136
Db 700 ACCGAGCGGTCTCATACCGGGCCACAGCGGTGACACGGCGGCGGCGAGTGGCGAAGATG 759
QY 137 ValAlaValTyrIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 760 CTGCTGTGTGGGTGTGGCTCTCTCTGTGTACGACGACCATCTCTG-----AGC 810
QY 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 811 TGGAGTACCTGTCCGGGGGCGAGCTCATCCCGAGGGCCACTGCTATGCCGAGTTCTTC 870
QY 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
Db 871 TACAACCTGGTACTTCTCTCATCAGCGCTTCACCGCTGGAGTTCTTACGCCCTTCTCTCAGC 930
QY 192 ValValTyrPheSerValGlnIleTyr----- 200
Db 931 GTCACTCTCTTAACCTCAGCATCTACTGAACATCAGAGGGCGACCCGCTCCGGCTG 990
QY 200 ----- 200
Db 991 GATGGGGCTCAGAGGCGAGCGGGCCCGAGCCCTCCCGAGGCCCGACCTCACACCC 1050
QY 201 -----TyrSerLeuTrpLysArgGlySerLeuSerArgCysProSerHis 215
Db 1051 CCACCGCTGGCTGCTGGGCTGTGTGCAGAGGGGCGACGGGAGGCGCATGCCGTGCAC 1110
QY 216 -----AlaGlyPheIleAlaThrSerSer 223
Db 1111 AGTATGGGTGGGTGAGGGCGCGTAGGGCTGAGCGCGGGAGGCGACCTCGGGGT 1170
QY 224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
Db 1171 GCGGTGGGGGGCGGCTCC-----GTGGCTTCAACCCACCTCCAGCTCCGGC--- 1215
QY 244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuVal 263
Db 1216 -----AGTCTCTCGAGGGGCACTGAGAGGGCGGCGC----- 1245
QY 264 SerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySerPheCysArg 283
Db 1246 -----TCACTCAAGAGGGGCTCAAAGCGGTGC 1272
QY 284 SerGluSerProValLeuHisGlnArg-----GluHis 294
Db 1273 GCGTCTCGGCTCTCACTGGAGAGCGCATGAGATGGTGTCCAGAGCTTCAACCCAGCGC 1332
QY 295 ValGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuSerAlaPhe 314
Db 1333 TTTCGGCTGTCTGGGACAGAAAGTGCAGTGCCTGCGCTCATCGTGCAGCATCTTT 1392
QY 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
Db 1393 GGGCTGTGTGGGCCCCATACACGTCTGTATGATCATCGGCGCGGCTC---CATGGC 1449
QY 335 GluArgProLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
Db 1450 CACTGCGTCCCTGACTACTGTGTACGAAACCTCTCTTGGCTCTGTGGGCGCAACTCGGCT 1509
QY 355 IleAsnProPheLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIle 374
Db 1510 GTCAACCTCTCTCTACCTCTGTGTCCACACAGCTTTCGCGGGCGCTTCAACAGCTG 1569
QY 375 LeuCysValThrLys-----GlnProAlaProSer 384
Db 1570 CTCTGCCCCAGAGAGCTCAAAATCCAGCCCGCCACAGCTCC 1608
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RESULT 12

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US-08-985-090-1
; Sequence 1, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-08-985-090-1

Alignment Scores:
Pred. No.: 2,59e-60 Length: 2689
Score: 693.00 Matches: 163
Percent Similarity: 49.2% Conservative: 50
Best Local Similarity: 37.6% Mismatches: 124
Query Match: 33.9% Indels: 96
DB: 2 Gaps: 11

US-10-626-126-9 (1-391) x US-08-985-090-1 (1-2689)
QY 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAlaValIle 37
Db 399 CTGGCGCGCTCATGCGCTGCTCATGCGGCACCGTGTGGCCACGCGTGTGTCATG 458
QY 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 459 CTGCGCTTGTGGCGGACTCGAGCTCCGCGACCCAGACCACTTCTTCTGCTCAACCTC 518
QY 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
Db 519 GCCATCTCCGACTTCTCTGTCGCGCGCTTCTGCATCCCACTGTATGTACCTAGTGTG 578
QY 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 579 ACAGGCGCTGGACCTTCGGCGCGGCGCTTGCAGCTGTGGTGTGGTAGTGAGTACCTG 638
QY 97 LeuCyThrAlaSerValTyrSerIleValIleSerTyrAspArgTyrGlnSerVal 116
Db 639 CTGTGACCTCTCTCTGCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGTGGTC
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117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyLeuLysIleValAlaGlnMet 136
   :::::::::::::::::::::::::::::
699 ACCGAGCGGTCTCATACCGGCCAGAGGGTGACACGGCGGCGAGTGCAGAGATG 758
   ::::::::::::::::::::::::::::::

137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
   ::::::::::::::::::::::::::::
759 CTGCTGTGGGTGTGGCTTCTCTGCTGTACGACGACCATCTG-----AGC 809

157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
   ::::::::::::::::::::::::::::
810 TGGGAGTACTGTCCGGGGGCGACTTCATCCCGAGGGCCACTGCTATGCCGAGTTCCTC 869

172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
   ::::::::::::::::::::::::::::
870 TACAACCTGGTACTCTCTCATCAGCGGTCTCACCTGGAGTCTTTAGCGCTTCTCTCAGC 929

192 ValValTyrPheSerValGlnIleTyr----- 200
   ::::::::::::::::::::::::::::
930 GTCACTTCTTTAACTCAGCATCTACTGAACATCCAGAGGGCCACCGCCTCCGGCTG 989

200 ----- 200

990 GATGGGGCTCAGAGGCGCGCGCCCGAGCCCTCCCGAGGCCCGACCTCACCACCC 1049

201 -----TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHis 215
   ::::::::::::::::::::::::::::
1050 CCACCGCTGGCTGTGGGCTGTCTGGCAGAGGGGCGACGGGAGGCCATGCGCTGCAC 1109

216 -----AlaGlyPheIleAlaThrSerSer 223
   ::::::::::::::::::::::::::::
1110 AGGTATGGGTGGGTGAGGGCGCGGTAGGGCTGAGCGCGGGGAGCGACCTCCGGGGT 1169

224 ArgGlyThrCysHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
   ::::::::::::::::::::::::::::
1170 GCGCGTGGGGCGGCTCC-----GTGGCTTCACCCACCTCCAGCTCCGGC--- 1214

244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuVal 263
   ::::::::::::::::::::::::::::
1215 -----AGTCTCTCGGGGCGACTGAGGCGCGGC----- 1244

264 SerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySerPheCysArg 283
   ::::::::::::::::::::::::::::
1245 -----TCACTCAAGAGGGGCTCCAAGCGGTG 1271

284 SerGluSerProValLeuHisGlnArg-----GluHis 294
   ::::::::::::::::::::::::::::
1272 GCGTCTCGGCTCTCACTGGAGAGCGCATGAAGATGGTGTCAGAGCTTCACCCAGCGC 1331

295 ValGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuSerAlaPhe 314
   ::::::::::::::::::::::::::::
1332 TTTCGGGTGTCTCGGNACGAAAGTGCCAGTCTGCTGGCCCTCATCGAGCATCTTT 1391

315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
   ::::::::::::::::::::::::::::
1392 GGGCTCTGTGGGCCCCATACACGCTGCTGATGATCATCGGCGCGCTC---CATGGC 1448

335 GluArgProLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
   ::::::::::::::::::::::::::::
1449 CACTGCTCTCCCTACTACTGTGTGCAAAACCTCTCTGCTCTGTGGCCAACTCGGCT 1508

355 IleAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
   ::::::::::::::::::::::::::::
1509 GTCAACCTGTCTCTTACCTCTGTGCCACACAGCTTCCGCGGGGCTTCACCAAGCTG 1568

375 LeuCysValThrLys-----GlnProAlaProSer 384
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1569 CTCTGCCCCAGAGGCTCAAAATCCAGCCCCACAGCTCC 1607
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RESULT 13

US-09-165-543-1

; Sequence 1, Application US/09165543

; Patent No. 6093545

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GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 291..1625
US-09-165-543-1

Alignment Scores:
Pred. No.: 2,59e-60 Length: 2689
Score: 693.00 Matches: 163
Percent Similarity: 49.2% Conservative: 50
Best Local Similarity: 37.6% Mismatches: 124
Query Match: 33.9% Indels: 96
DB: 3 Gaps: 11

US-10-626-126-9 (1-391) x US-09-165-543-1 (1-2689)

QY 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValle 37
   ::::::::::::::::::::::::::::
Db 399 CTGGCGCGCTCATGCGCTGCTCATGTCGGCCACCGGTCTGGCCACGCGCTGGTCATG 458

QY 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
   ::::::::::::::::::::::::::::
Db 459 CTGCGCTTCTGGCCGACCTCGAGCTCCGACCCAGACCACTCTCTCTCTCTCACTC 518

QY 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
   ::::::::::::::::::::::::::::
Db 519 GCCATCTCCGACTCTCTGTCGGCGCTTCTGTCATCCCACTGATGTACCTACGTCGTG 578

QY 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
   ::::::::::::::::::::::::::::
Db 579 ACAGCGCGCTGGACCTTCGCGCGCGGCTCTGCAAGCTGTGGCTGTGTAGTGAGTACTG 638

QY 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
   ::::::::::::::::::::::::::::
Db 639 CTGTGACCTCTCTGCTCCATCGTGTCTCATCAGCTACGACCGCTTCTCTCTGCGTGC 698

QY 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMet 136
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Db 699 ACCGAGCGGTCTATACCGGCGCCAGAGGGTGACAGCGGGCGAGTCCGGAAGATG 758
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 759 CTGCTGGTGTGGGTCTCTGCTGTACGACGACGACCATCTG-----AGC 809
Qy 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 810 TGGAGTACCTGTCCGGGGCGGACGTCCATCCCGAGGGCCACTGATGCCGAGTTCTTC 869
Qy 172 ThrGluTrpTrpIleLeuAlaPheLeuGluPheLeuLeuProValSerLeu 191
Db 870 TACAACCTGGTACTCTCTCATCGCTTCCACCTGGAGTTCTTACGCCCTTCTCAGC 929
Qy 192 ValValTrpPheSerValGlnIleTyr----- 200
Db 930 GTACACCTTCTTAACCTCAGCATCTACCTGAACATCCAGAGCGCACCGCGCTCCGGGTG 989
Qy 200 ----- 200
Db 990 GATGGGCTCGAGAGCGACCGCGCCCGAGCCCTCCCGAGGCCACGCTCCACACCC 1049
Qy 201 -----TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHis 215
Db 1050 CCACCGCTGCTGCTGGGGCTGTGGCAGAAGGGGACAGGGGAGCGCATGCCCTGCAC 1109
Qy 216 -----AlaGlyPheIleAlaThrSerSer 223
Db 1110 AGGTATGGGTGGGTAGGCGCGGTAGCGCTCAGCGCGGGGAGCGACCTCGGGGT 1169
Qy 224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
Db 1170 GCGGTCTGGGGCGGCTCC-----GTGGCTTCACCCACCTCCAGTCCGGC--- 1214
Qy 244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuVal 263
Db 1215 -----AGCTCTCGAGGGGCACGTGAGGCGCGGC----- 1244
Qy 264 SerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySerPheCysArg 283
Db 1245 -----TCACCTCAGAGGGGTCCAGCCGCTG 1271
Qy 284 SerGluSerProValLeuHisGlnArg-----GluHis 294
Db 1272 GCGTCTCGGCTCCTCCTGAGAGAGCGCATGAAGATGGTGTCCAGAGCTTCACCCAGCGC 1331
Qy 295 ValGluLeuLeuArgGlyArgGlyLeuAlaArgSerLeuAlaValLeuLeuSerAlaPhe 314
Db 1332 TTTCGGCTGTCTCGGGACAGGAAGTGGCCAAAGTCGCTGGCCGTCATCGTGAGCATCTTT 1391
Qy 315 AlaIleCysTrpAlaProTyrCysPhePheThrIleValLeuSerThrTyrArgGly 334
Db 1392 GGGCTGTCTGGGCGCCCATACACGCTGCTGATGATCATCCGGCGCGCTGC---CATGGC 1448
Qy 335 GluArgProLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
Db 1449 CACTGCTCCCTGACTACTGTGTACAAACCTCTCTCTGGCTCTGTGGGCAACTCGGCT 1508
Qy 355 IleAsnProPheLeuTrpProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
Db 1509 GTCAACCTGTGCTCTACCTCTGTGTCACACACAGCTTCGCGCGGGCTTCACCAAGCTG 1568
Qy 375 LeuCysValThrLys-----GlnProAlaProSer 384
Db 1569 CTCTGCCCCCAGAGCTCAAAATCCAGCCGCCACAGCTCC 1607
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RESULT 14

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US-09-167-354-5
; Sequence 5, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
```

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; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-167-354-5
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Alignment Scores:
Pred. No.: 2,6e-60 Length: 2699
Score: 693.00 Matches: 163
Percent Similarity: 49.2% Conservative: 50
Best Local Similarity: 37.6% Mismatches: 124
Query Match: 33.9% Indels: 96
DB: 3 Gaps: 11

US-10-626-126-9 (1-391) x US-09-167-354-5 (1-2699)
Qy 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIle 37
Db 407 CTGGCGCGCTCATGGCGCTGCTCATGTCGCCACGGTGTGGGCAACGCGCTGTCTCATG 466
Qy 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 467 CTGCGCTCTGTGGCGGACTCGAGCTCCGCCACCGACCAACAACATCTCTCTCTCAACCTC 526
Qy 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrIleu 77
Db 527 GCCATCTCCGACTCTCTGTCGCGCGCTTCTGCATCCCACTGTATGTATACCTACGTGCTG 586
Qy 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrIleu 96
Db 587 ACAGGCGCTGGACCTTCGGCGGGGCTCTGCAAGCTGTGGTGTAGTGGACTACCTG 646
Qy 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 647 CTGTGCACTCTCTGCTTCAACATCGTCTCATCAGCTACGACCGCTTCTCTCTCGCTC 706
Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMet 136
Db 707 ACCGAGCGGCTCTCATACCGGGGCCACAGGGGTGACACGCGGGCGGCGAGTGCAGAAATG 766
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 767 CTGCTGTGTGGTGTGGCTTCTCTGCTGACGACGACGACCATCTCTG-----AGC 817
Qy 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 818 TGGAGTACCTGTCTCGGGCGGACGCTCCATCCCGAGGGCCACTGCTATGCGAGTTCTTTC 877
Qy 172 ThrGluTrpTrpIleLeuAlaIleThrAlaPheLeuGluPheLeuLeuProValSerLeu 191
Db 878 TACAACCTGGTACTTCTCTCATCGGCTTCCACCTGGAGTTCTTTTACGCCCTTCTCAGC 937
Qy 192 ValValTrpPheSerValGlnIleTyr----- 200
Db 938 GTACACCTTCTTAACCTCAGCATCTACCTGAACATCCAGAGGGCACCGCGCTCCGGCTG 997
Qy 200 ----- 200
Db 998 GATGGGCTCGAGAGGCGCGCGCGCCCGCTCCCGAGGCCACGCTCCACACCC 1057
Qy 201 -----TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHis 215
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Db      1058 CCACCGCTGGCTGGGCTCTGGCAGAGGGGACGGGAGGCCATCGCGCTGCAC 1117
Qy      216 -----AlaGlyPheIleAlaThrSerSer 223
Db      1118 AGGTATGGGTGGGTGAGCGCGCTAGGCGCTGAGCGCGGGAGCGACCTCGGGGGT 1177
Qy      224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
Db      1178 GCGGGTGGGGCGGCTCC-----GTGGCTTCACCCACCTCCAGCTCCGGC--- 1222
Qy      244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerLeuLeuVal 263
Db      1223 -----AGCTCTCGAGGGGCACTGAGAGCGCGGC----- 1252
Qy      264 SerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySerPheCysArg 283
Db      1253 -----TCACTCAAGAGGGGCTCCAAAGCGGTGC 1279
Qy      284 SerGluSerProValLeuHisGlnArg-----GluHis 294
Db      1280 GCGTCTCGGCTCGCTGGAGAGCGCATGAAGTGTGCCAGAGCTTCACCCAGCGC 1339
Qy      295 ValGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPhe 314
Db      1340 TTTCGGCTGTCTCGGACAGGAAGTGCCTCAAGTGTGCGCTCATCGTGAGCATTTT 1399
Qy      315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
Db      1400 GGGCTGTCTGGGCCCCATACACGCTGCTGATGATCATCGGCGCGCTGC---CATGGC 1456
Qy      335 GluArgProLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
Db      1457 CACTGGCTCCTGACTACTGGTACGAAACCTCTCTTGGCTCTGTGGGCGCAACTCGGCT 1516
Qy      355 IleAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
Db      1517 GTCAACCTGTCTCTACCTCTGTGCCACACACAGCTTCGCGCGGCGCTTCACCAAGCTG 1576
Qy      375 LeuCysValThrLys-----GlnProAlaProSer 384
Db      1577 CTCTGCCCCGAGAAGCTCAAAATCCAGCCCCACAGCTCC 1615

RESULT 15
US-09-642-855-5
; Sequence 5, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; PRIOR FILING DATE: 2000-08-21
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-5

Alignment Scores:
Pred. No.: 2,6e-60 Length: 2699
Score: 693.00 Matches: 163
Percent Similarity: 49.2% Conservative: 50

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Best Local Similarity: 37.6% Mismatches: 124
Query Match: 33.9% Indels: 96
DB: 3 Gaps: 11

US-10-626-126-9 (1-391) x US-09-642-855-5 (1-2699)

Qy      18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIle 37
Db      407 CTGGCCGCGCTCATGGCGTGTCTCATCGTGGCCACCGTGTGGCAACGCGTGGTGCATG 466
Qy      38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db      467 CTGCGCTCTGTGGCCGACTCGAGCTCCGACCCAGACAACTTCTTCCTGCTCAACCTC 526
Qy      58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
Db      527 GCATCTCCGACTTCTCTGTCGGCGCTTCTGTCATCCCACTGATGATGACTACGTGCTG 586
Qy      78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db      587 ACAGGCGCGCTGGACCTTCGGCCGGGCGCTCTGCAAGCTGTGGTGTAGTGAGTACCTG 646
Qy      97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db      647 CTGTGCACCTCTCTCTGCTTCAACATCGTGTCTCATGAGCTACGACCGCTTCTGTGCGTC 706
Qy      117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMet 136
Db      707 ACCGAGCGGTCTCATACCGGGCCAGCAGGGTGACACGGCGGGGAGTGCGGAGATG 766
Qy      137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db      767 CTGCTGGTGTGGTGTCTGCGCTTCTGCTCTACGACCGACCGCATCTCTG-----AGC 817
Qy      157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db      818 TGGGAGTACTGTCTCGGGGGCGACCTCATCCCGAGGGCCACTGTATGCGAGTTCTTC 877
Qy      172 ThrGluTrpTrpIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
Db      878 TACAATGGTACTTCTCTCATCGGCTTCCACCTGGAGTTCTTTAGGCCCTTCTCTCAGC 937
Qy      192 ValValTyrPheSerValGlnIleTyr----- 200
Db      938 GTACCTCTTTAACTCATGCACTTACTGAACATCCAGAGGGCGACCCGCTCCGCGCTG 997
Qy      200 ----- 200
Db      998 GATGGGCTCGAGAGGCGAGCGCGCCCGAGCCCTCCCGAGGCCCGCCCTCACCAACC 1057
Qy      201 -----TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHis 215
Db      1058 CCACCGCTGGTGTCTGGGGCTCTGCGAGAAGGGGACCGGGAGGCGCATGCGCTGCAC 1117
Qy      216 -----AlaGlyPheIleAlaThrSerSer 223
Db      1118 AGGTATGGGTGGGTGAGCGCGCTAGGCGCTGAGCGGGGAGCGACCTCGGGGGT 1177
Qy      224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
Db      1178 GCGGTGGGGCGGCTCC-----GTGGCTTCACCCACCTCCAGCTCCGGC--- 1222
Qy      244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerLeuLeuVal 263
Db      1223 -----AGCTCTCGAGGGGCACTGAGAGCGCGGC----- 1252
Qy      264 SerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySerPheCysArg 283
Db      1253 -----TCACTCAAGAGGGGCTCCAAAGCGGTGC 1279
Qy      284 SerGluSerProValLeuHisGlnArg-----GluHis 294
Db      1280 GCGTCTCGGCTCGCTGGAGAGAGCGCATGAAGTGTGCCAGAGCTTCACCCAGCGC 1339

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Qy 295 ValGluLeuLeuArgGlyArgGlyLeuAlaArgSerLeuAlaValLeuLeuSerAlaPhe 314
Db 1340 TTTCGGGTGCTCGGGACAGGAAAGTGGCCAAAGTCGCTGGCCGTCATCGTGAGCATCTTT 1399
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
Db 1400 GGGCTCTGCTGGGCCCCCATACACGCTGCTGATGATCATCCGGCGCGCTGC---CATGGC 1456
Qy 335 GluArgProLysSerIleTTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
Db 1457 CACTGCGTCCCTGACTACTGTACGAAACCTCTCTGGCTCTCTGGGCCCACTCGGCT 1516
Qy 355 IleAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpIle 374
Db 1517 GTCAACCCCTGCTCTACCCCTCTGTGCCACCACACAGCTTCGCGCGGCTTCACCAAGCTG 1576
Qy 375 LeuCysValThrLys-----GlnProAlaProSer 384
Db 1577 CTCGCCCCCAGAGACTCAAAATCAGCCCCACAGTCC 1615
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Job time : 262 secs

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GenCore version 5.1.7
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Run on: April 29, 2006, 01:58:11 ; Search time 861 Seconds

(without alignments)

3755.316 Million cell updates/sec

Title: US-10-626-126-9

Perfect score: 2045

Sequence: 1 MSESNGTDVLPPLTAQVPLAF.....WKILCVTKQAPSQTSVSS 391

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2034	99.5	1176	8	US-10-626-445-6 Sequence 6, Appli
2	2034	99.5	1176	9	US-10-626-126-6 Sequence 6, Appli
3	2034	99.5	1176	9	US-10-626-398-6 Sequence 6, Appli
4	1742	85.2	1176	8	US-10-626-445-5 Sequence 5, Appli
5	1742	85.2	1176	9	US-10-626-126-5 Sequence 5, Appli
6	1742	85.2	1176	9	US-10-626-398-5 Sequence 5, Appli
7	1403.5	68.6	1170	9	US-10-488-421-7 Sequence 7, Appli

8	1403.5	68.6	1173	3	US-09-812-216-1	Sequence 1, Appli
9	1403.5	68.6	1173	3	US-09-910-411-1	Sequence 1, Appli
10	1403.5	68.6	1173	3	US-09-875-076-13	Sequence 13, Appli
11	1403.5	68.6	1173	3	US-09-876-252-13	Sequence 13, Appli
12	1403.5	68.6	1173	5	US-10-052-193-1	Sequence 1, Appli
13	1403.5	68.6	1173	6	US-10-272-983-13	Sequence 13, Appli
14	1403.5	68.6	1173	6	US-10-354-769-1	Sequence 1, Appli
15	1403.5	68.6	1173	6	US-10-393-807-13	Sequence 13, Appli
16	1403.5	68.6	1173	6	US-10-417-820A-13	Sequence 13, Appli
17	1403.5	68.6	1173	7	US-10-349-253A-1	Sequence 1, Appli
18	1403.5	68.6	1173	7	US-10-723-955-13	Sequence 13, Appli
19	1403.5	68.6	1173	7	US-10-782-596-13	Sequence 13, Appli
20	1403.5	68.6	1173	7	US-10-737-619-1	Sequence 1, Appli
21	1403.5	68.6	1173	8	US-10-626-445-1	Sequence 1, Appli
22	1403.5	68.6	1173	9	US-10-616-088-1	Sequence 1, Appli
23	1403.5	68.6	1173	9	US-10-626-126-1	Sequence 1, Appli
24	1403.5	68.6	1173	9	US-10-626-398-1	Sequence 1, Appli
25	1403.5	68.6	1173	9	US-10-723-955-13	Sequence 13, Appli
26	1403.5	68.6	1266	3	US-09-891-138A-5	Sequence 5, Appli
27	1403.5	68.6	1300	3	US-09-852-165-1	Sequence 1, Appli
28	1403.5	68.6	1300	7	US-10-696-673-1	Sequence 1, Appli
29	1403.5	68.6	3689	5	US-10-225-567A-628	Sequence 628, App
30	1403.5	68.6	3689	8	US-10-684-206-19	Sequence 19, Appli
31	1403.5	68.6	3689	9	US-10-756-149-32	Sequence 32, Appli
32	1398.5	68.4	1173	6	US-10-290-078-26	Sequence 26, Appli
33	1398.5	68.4	1265	6	US-10-290-078-25	Sequence 25, Appli
34	1398.5	68.4	1265	9	US-10-488-421-5	Sequence 5, Appli
35	1237.5	60.5	1170	8	US-10-626-445-7	Sequence 7, Appli
36	1237.5	60.5	1170	9	US-10-626-126-7	Sequence 7, Appli
37	1237.5	60.5	1170	9	US-10-626-398-7	Sequence 7, Appli
38	1233	60.3	1166	9	US-10-488-421-3	Sequence 3, Appli
39	1117.5	54.6	1103	9	US-10-488-421-1	Sequence 1, Appli
40	693	33.9	1335	3	US-09-350-206-3	Sequence 3, Appli
41	693	33.9	1335	3	US-09-349-755-3	Sequence 3, Appli
42	693	33.9	1335	5	US-09-166-334-3	Sequence 3, Appli
43	693	33.9	1335	5	US-10-282-958-3	Sequence 3, Appli
44	693	33.9	1335	7	US-10-727-021-6	Sequence 6, Appli
45	693	33.9	1335	10	US-11-059-105-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-10-626-445-6
; Sequence 6, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-445-6

Alignment Scores:
Pred. No.: 5.75e-215 Length: 1176
Score: 2034.00 Matches: 390
Percent Similarity: 99.7% Conservatives: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.5% Indels: 0
DB: 8 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-445-6 (1-1176)

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QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGTCGGAGTCTAAACGGCAGCTGCTTCCCACTGACTGCTCAAGTCCCTTTGGCATT 60
QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTAATGTCCTGCTTGCTTTGCTATACAGATAGGCAATGCTGTGGTCATTTTAGCCTTT 120
QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTAGCAGACAGAAACCTTACATCGAAGTAATATATTTTCTTAATTTGGCTATTCT 180
QY 61 AspPheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80
Db 181 GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCTCACAGCTGTTTAACTGG 240
QY 81 AsnProGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 AATTTTGGAAAGTGGAACTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCA 300
QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCCGTCTACAGTATTGTCCTCATTTAGCTACGATCGATACCAGTCAGTTTCAAACGCTGTG 360
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValAlaValTyr 140
Db 361 CGTTATAGACACAGCACACTGGCATCTCGAAATTTGTTGCTCAAAATGGTGGTGTGG 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160
Db 421 ATACTGGCTTCTTGTGTCATGCCCCAATGATTTCTGGCTTCGGATTTCTGGAGAACAGC 480
QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrIleLeuAlaIleThr 180
Db 481 ACCAACACAGAGGAGTGCAGAGCTGGCTTTGTTACTGAGTGGTACATCCTCGCCATTACA 540
QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 541 GCATTCTTGGAAATTCCTGCTCCCTGCTCTCTGCTGGTGTCTATTTTCAAGTGTACAGATTAC 600
QY 201 TrpSerLeuTyrLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 601 TGGAGCCTGTGGAAAGCTGGAGTCTCAGTAGGTGCCCTAGCCACCGCTGGATTCATCGCT 660
QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 661 ACCTCTTCCAGGGGCACCTGGACACTCACGCGAAGCTGGGTGGCTGTAGGACAAAGTCTT 720
QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 721 CCTGGATTAAAGGAACAGCGCATCCCTTCAVTCAGAAAAGTCCACGAGGAAAGAGCAGT 780
QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 781 CTCTGTGTGTCCTTAAGACTCACATGAGCGGTATGATCATCGCTTCAAAGTGGGTTC 840
QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 841 TTCTGCCGATCAGAAAGCCAGTCCTTCCACGAGAGAGCAGCTGGAGCTTCTCAGAGGC 900
QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTyrAlaPro 320
Db 901 AGGAAAGTAGCCAGTCCGTAGCTGTCTCTCAGTGTCTTTTGGCATTTTGTGGGTCCG 960
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 961 TATTGGCTGTTCACAATGTGTTCTTCAACATATTCGAGAGGGGAGGCCCCCAATCGATT 1020
QY 341 TrpTyrSerIleAlaPheTyrLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1021 TGGTACAGCATAGCCTTTTGGCTACAGTGGTTCAATTCATTTAATATCCCTTCTTATAC 1080
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QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTyrLysIleLeuCysValThrLysGln 380
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QY 381 ProAlaProSerGlnThrGlnSerValSerSer 391
Db 1141 CCAGCACCTTCACAGACCCAGTCAGTATCTTCT 1173
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RESULT 2

US-10-626-126-6
; Sequence 6, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-126-6

Alignment Scores:
Pred. No.: 5,75e-215 Length: 1176
Score: 2034.00 Matches: 390
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.5% Indels: 0
DB: 9 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-126-6 (1-1176)

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Db 1 ATGTCGGAGTCTAAACGGCAGCTGCTTCCCACTGACTGCTCAAGTCCCTTTGGCATT 60
QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTAATGTCCTGCTTGCTTTGCTATAACGATAGGCAATGCTGTGGTCATTTTAGCCTTT 120
QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTAGCAGACAGAAACCTTACATCGAAGTAATATATTTTCTTAATTTGGCTATTCT 180
QY 61 AspPheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80
Db 181 GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCTCACAGCTGTTTAACTGG 240
QY 81 AsnProGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 AATTTTGGAAAGTGGAACTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCA 300
QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCCGTCTACAGTATTGTCCTCATTTAGCTACGATCGATACCAGTCAGTTTCAAACGCTGTG 360
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
Db 361 CGTTATAGACACAGCACACTGGCATCTCGAAATTTGTTGCTCAAAATGGTGGTGTGG 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160
Db 421 ATACTGGCTTCTTGTGTCATGTCCTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTTGAAGAACAGC 480
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Qy	161	ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr	180
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Qy	181	AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr	200
Db	541	GCATTCCTGGAATTCCTGCTCCCTGCTCTCTCTGGTGGTCTATTTTCAGTGACAGATTTC	600
Qy	201	TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla	220
Db	601	TGGAGCCTGTGGAGCGTGGGAGTCTCAGTAGGTGGCTTAGCCACGCTGGATTTCATCGCT	660
Qy	221	ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu	240
Db	661	ACCTCTTCCAGGGCACCTGGACACTACGAGAACTGGGTGGCTTTGTAGACAAAGTCCT	720
Qy	241	ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer	260
Db	721	CCTTGGATTAAAGAAACCGCCGCATCCTTCATTCAGAAAGTCCACAGAGAAAGAGCAGT	780
Qy	261	LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer	280
Db	781	CTCTGTGTGCTTTAAGGACTCACATGAGCGGTAGTATCATCGCCTTCAAAGTGGGTTC	840
Qy	281	PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly	300
Db	841	TTCTGCCGATCAGAAAGCCAGTGTCTTCCACAGAGAGACGCTGGAGCTTCTCAGAGGC	900
Qy	301	ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro	320
Db	901	AGGAAGCTAGCAGGTGCTAGCTGTCTCTCTGAGTGTCTTTGGCATTTGCTGGGCTCCG	960
Qy	321	TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle	340
Db	961	TATTTGCCGTGTTCAAAATTGTTCTTTTCAACTTATCGAGAGGGAGCGCCCAAAATCGATT	1020
Qy	341	TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr	360
Db	1021	TGGTACAGCATAGCTTTTGGCTACAGTGGTTCAATTCATTTAATTCCTCTTCTATAC	1080
Qy	361	ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln	380
Db	1081	CCTTTGTGCCACAGACGTTTCCAGAGGCTTCTGGAGAGTACTCTCTGTGTGACAAAGCAA	1140
Qy	381	ProAlaProSerGlnThrGlnSerValSerSer	391
Db	1141	CCAGCACCTTTCACAGACCCAGTCAGTATCTCT	1173

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RESULT 3
US-10-626-398-6
; Sequence 6, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
; US-10-626-398-6

Alignment Scores:

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Alignment Scores:

Pred. NO.:	5.75e-215	Length:	1176
Score:	2034.00	Matches:	330
Percent Similarity:	99.7%	Conservative:	0
Best Local Similarity:	99.7%	Mismatches:	1
Query Match:	99.5%	Indels:	0
DB:	9	Gaps:	0

US-10-626-126-9 (1-391) x US-10-626-398-6 (1-1176)

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Db	1	ATGTCGGAGCTTAACGGCACTGACGCTCTGGCACTGACTGCTCAAGCTCCCTTGGCAATTT	60
Qy	21	LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe	40
Db	61	TTAATGTCCTCTGCTTTTTCGTATACGATAGCAATGCTGTGCTCATTTTAGCCTTT	120
Qy	41	ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer	60
Db	121	GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT	180
Qy	61	AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp	80
Db	181	GACTTCTTCTGGTGGTGCATCTCCATTCCTCTGTATACCTCCCTCACACGCTGTTAACTGG	240
Qy	81	AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla	100
Db	241	AAATTTTGAAGTGAATCTGCATGTTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCA	300
Qy	101	SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal	120
Db	301	TCCGCTACAGTATTGTCTCTCATTAGCTACGATCGATACCACTCAGTTTCAAACGCTGTG	360
Qy	121	ArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValAlaValTrp	140
Db	361	CGTTATAGACACACAGCACACTGGCATCTCGAAAATTGTTGCTCAAATGGTGGCTGTTTGG	420
Qy	141	IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIleValSer	160
Db	421	ATACTGGCTTTCTTGGTCAATGGCCCAATGATTCGGCTTCGGATTCTTGGAGAACAACGC	480
Qy	161	ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr	180
Db	481	ACCAACACAGAGGAGTGGACCTGGCTTTGTTACTGAGTGGTACATCTCTGCCATTACA	540
Qy	181	AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr	200
Db	541	GCATTTCTTGGAAATTCCTGCTCCCTCTCTCTCTGGTGGTCTATTTTTCAGTGTACAGATTTAC	600
Qy	201	TrpSerLeuTrpIleValArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla	220
Db	601	TGGAGCTTGTGGAAAGCGTGGAGATCTCAGTAGGTGCCCTTAGCCACGCTGGATTATCGCT	660
Qy	221	ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu	240
Db	661	ACCTCTCTCCAGGGGCACTGGACACTCACGCAAGACTGGGTTGGCTTGTAGGACAAAGTCTT	720
Qy	241	ProGlyLeuIleValGluProAlaAlaSerLeuHisSerGluSerProArgGlyIleValSer	260
Db	721	CCTGGATTTAAAGGAACCAACGCGCATCCCTTCATTCCAGAAAGTCCACAGAGAAGAGCAGT	780
Qy	261	LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheIleValGlySer	280
Db	781	CTCTCTGGTGTCTTTAAGGACTCACATGACGGGTAGTATCATCGCTTCTCAAGTGGGTTC	840
Qy	281	PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly	300
Db	841	TTCTCCCGCATCAGAAAGCCAGTGTCTTCAACAGAGAGACACGCTGGAGCTTCTCAGAGGC	900
Qy	301	ArgIleValAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro	320
Db	901	AGGAAGCTTAGCAGTCCGCTAGTCTCTCTCTGAGTGTCTTTGGCAATTTGCTGGGCTCG	960

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Qy 321 TycCysLeuPheThrIleValLeuSerThrTyArgArgGlyGluArgProLysSerIle 340
Db 961 TAITGCGCTGTTCAAAATGTTCTTCAACTATTCGACAGGGGAGCGCCCAAAATCGAAT 1020

Qy 341 TtpTyrSerIleAlaPheTlpLeuGlnTlpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1021 TGGTACAGCATAGCCTTTTGGCTACAGTGGTTCATTTCACTTATTAATCCCTTTCTATAC 1080

Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTlpLysIleLeuCysValThrLysGln 380
Db 1081 CCTTTGGCCACAGACGTTTCCAGAGGCTTTCTGGAGATACCTCTGTGTGACAAAGCAA 1140

Qy 381 ProAlaProSerGlnThrGlnSerValSerSer 391
Db 1141 CCAGCACCTTCACAGACCCAGTCAGTATCTTCT 1173

RESULT 4
US-10-626-445-5
; Sequence 5, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-445-5

Alignment Scores:
Pred. No.: 1,5e-182 Length: 1176
Score: 1742.00 Matches: 332
Percent Similarity: 89.3% Conservative: 17
Best Local Similarity: 84.9% Mismatches: 42
Query Match: 85.2% Indels: 0
DB: 8 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-445-5 (1-1176)

Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGTGGAGGCTAACAGTACTGCATCTGCCACCGAGTCTCAGGTCCTCCCTGGCATTT 60

Qy 21 LeuMetSerLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTAATGCTTCAATTTGCTTTGCTATAATGCTAGGCAATGCTGTGTGTCATCTTAGCCTTT 120

Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTATTTTCTTAATTTGGCTATTTCT 180

Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrIleLeuPheAsnTlp 80
Db 181 GACTTCTCGTGGGTGTGATTTCAATTCCTCTGTGTACATCCCTCAGCTGTTGTTAACTGG 240

Qy 81 AsnProGlySerGlyIleCysMetPheTlpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCATTACTGACTATCTTTTGTGACCGCA 300

Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTCTACAATAATTGTCTCTCATTAGCTACGATCGATACAGTCAGTTTCAAAATGCTGTG 360
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Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTlp 140
Db 361 TCTTATAGGCTCAACACACATCGCATCATGAAGATTTGTGCTCAAAATGGTGTGTTGG 420

Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTlpLysAsnSer 160
Db 421 ATACTGGCTTTCTTGTGTAATAGCCCGATGATTTCTGGCTTCAGATTTCTTTGGAAGAACAGC 480

Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTlpTyrIleLeuAlaIleThr 180
Db 481 ACGAACACAAAGGACTGTGAGCTGGCTTTGTTCAGAGTGGTACATCTCCACATTACA 540

Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 541 ATGCTCTTGGAAATTCCTGCTTCTGTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTAC 600

Qy 201 TlpSerLeuTlpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTTCTCCACT 660

Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 661 ACCTTTCAGTGTTCAGACACACTTACACAGAGTGGGTGGCTTGCAGGACAAATAAT 720

Qy 241 ProGlyLeuLysGluProAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 721 CCTGGATTCGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCGAAGAAAGAGCAGC 780

Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 781 ATCTGTGTCTTAAAGGACTCAGTCACTGAAACAGCAGTATCAGTCCCTTCAAGTGGGTTC 840

Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 841 TTCTGGCATCGAAAGTGCAGCGCTTCGCCAAAGGAGTACGACAGAGCTTCTCAGAGGC 900

Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTlpAlaPro 320
Db 901 AGGAAGCTAGCCAGGTCAGTGGCCATCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960

Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 961 TACTGTCTTTCACAAATGCTCTTCACTTACCCAGAACCGAAGCGCCCAAAATCGGTG 1020

Qy 341 TtpTyrSerIleAlaPheTlpLeuGlnTlpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1021 TGTACAGCATTTGCCCTTCTGGCTGCATGTTCAATTCGTTTGTATCCCTTCTGTATC 1080

Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTlpLysIleLeuCysValThrLysGln 380
Db 1081 CCTTTGTGTACAGGCGTTTCCAGAGGCTTTCTGGAAGATACTTTGTGTGACAAAGCAA 1140

Qy 381 ProAlaProSerGlnThrGlnSerValSerSer 391
Db 1141 CCAGCGCTGTCAAGAACCCAGTCAGTATCTTCT 1173

RESULT 5
US-10-626-126-5
; Sequence 5, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-126-5

Alignment Scores:
Pred. No.: 1.5e-182 Length: 1176
Score: 1742.00 Matches: 332
Percent Similarity: 89.3% Conservativity: 17
Best Local Similarity: 84.9% Mismatches: 42
Query Match: 85.2% Indels: 0
DB: 9 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-126-5 (1-1176)

Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGTGGAGTCTAACAGTACTGGCATCTTGCACCCAGCTGCTCAGGTCCCTTGGCATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTAATGCTCTTCATTTGGCTTTGCTATTAATGGTAGGCAATGCTGTGTCATCTTAGCCTTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCTTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80
Db 181 GACTTCTGTGGTGTGATTTCCATCTCTGTATACCTCCCTCAGTGTGTGTTAACTGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 AATTTTGGAGTGGATCGCATCTTGTGCTCACTTACTGACTATCTTTTGTGCACCGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTCTACAATATGCTCTCATTTAGTACGATCGATACCATCAGTCTGAGTTTCAAAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuValIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATGTTGCTCAAAATGGTGGCTGTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIleAsnSer 160
Db 421 ATACTGGCTTCTTGTGTAATGGCCGCGATGATCTGGCTTCAGATCTTGGAGNACAGC 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 ACGAACACAAAGAGCTGTGAGCTGGCTTTGTTACAGAGTGTATCATCTCACCAATTACA 540
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 541 ATGCTCTTGGAAATCTCTGCTCTCTGTCATCTCTGTGGCTTATTTCAATGTATCAGATTTAC 600
Qy 201 TrpSerLeuTrpIleAspGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 601 TGGAGCTGTGGAGAGGTAGGGCTCTCAGTAGTGGCCCTAGGCATGCTGGATTTCCACT 660
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 661 ACCTCTTCCAGTCTTCCAGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720
Qy 241 ProGlyLeuIleGluProAlaAlaSerLeuHisSerGluSerProArgIleYysSerSer 260
Db 721 CCTGGATTGAAGAAATCAGCTGCTATCTGCTCATCTCAGAAAGTCCCTCGAAGAAAGACGAGC 780
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheIleValGlySer 280
Db 781 ATCTGTGTGTCCTTAAGGACTCACATGAACAGCAGTATCATCTGCCCTTCAAAAGTGGGTTC 840
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300

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Db 241 AATTTTGGAGTGGAACTCTGCATGTTTGGCTCATTACTGACTATCTTTGTGCGCCGCA 300
Qy SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTCTACAAATATGTCCTCATGTAGCTAGCATGATACCAGTCAGTTTCAAAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGGCTCAACACATGGCATCATGAGATTGTTGCTCAATGGTGGCTGTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 ATACTGGCTTCTTGGTAATGCCCGCATGATCTCTGGCTTATTTCAATGTACAGTTTAC 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 ACGAACACAAAGGACTGTGAGCTGGCTTTGTACAGAGTGGTACATCTCCACATTACA 540
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 541 ATGCTCTTGGAAATCTCTGCTTCTGTCTCATCTCTGTGGCTTATTTCAATGTACAGTTTAC 600
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 601 TCGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTCTCCACT 660
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 661 ACCTCTCCAGTGCTTACAGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT 720
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 721 CTTGGATTGAAGNATCAGCTGATCTCGTCACTCAGAAAGTCTTCGAGAAAGAGCAGC 780
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 781 ATCTGTGTGCTTAAAGACTCACATGACAGCAGTATCACTGCCTTCAAAAGTGGGTCC 840
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 841 TTTTGGCGATCGGAAAGTGCGAGCGCTTCGCCAAAGGGAGTACGCGAGAGCTTCTCAGAGGC 900
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 901 AGAAGCTACCGAGTCACTGGCCATCTTCTGAGCGCTTTTGGCATTTGCTGGGTCCA 960
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 961 TACTGTCTGTTCAAAATGTCCTTTCAACTTACCCAGAACGGAACGCCCAAAATCGGTG 1020
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1021 TGGTACAGCATGCTCTCTGGCTGCAATGGTTCAAATTCGTTTGTAAATCCCTTTCTGTAC 1080
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1081 CCTTTGTGTCAGGCGCTTTCAGAGGCGCTTCTGGNAGATACTTTGTGTGACAAAGCAA 1140
Qy 381 ProAlaProSerGlnThrGlnSerValSerSer 391
Db 1141 CCAGCGCTGTACAGAACCAAGTCAGTATCTTCT 1173
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RESULT 7

US-10-488-421-7

; Sequence 7, Application US/10488421

; Publication No. US20050239065A1

; GENERAL INFORMATION:

; APPLICANT: Merck & Co., Inc. [US/US]

; APPLICANT: Gallagher, Michael J.

; APPLICANT: Yates, Stephen L.

; TITLE OF INVENTION: HISTAMINE RECEPTOR H4 POLYNUCLEOTIDES

; FILE REFERENCE: 1367-13335W001

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; CURRENT APPLICATION NUMBER: US/10/488,421
; CURRENT FILING DATE: 2004-03-01
; PRIOR APPLICATION NUMBER: US 60/316,762
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/332,697
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1170)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: H4SEQMORSE - Genbank Accession No. AF329449
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Morse, et al., JPET 296(3):1058-1066 (2001); U.S. Patent
; OTHER INFORMATION: No. 6,204,017; WO 01/25432 A2
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Liu - Genbank Accession No. AF312230 - Liu et al., Mol.
; OTHER INFORMATION: Pharmacol 59(3):420-426 (2001)
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Banyu - Genbank Accession No.: AB045370; WO 01/46414 A1
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Nguyen, et al., Mol. Pharmacol 59(3):427-433 (2001) a.a. sequence
; OTHER INFORMATION: are AAG and 988 is C
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Jones - Genbank Accession No.: AF307973; Nucleotides 460-462
; OTHER INFORMATION: are AAG and 988 is C
; US-10-488-421-7
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Alignment Scores:
Pred. No.: 5,68e-145 Length: 1170
Score: 1403.50 Matches: 271
Percent Similarity: 79.3% Conservative: 40
Best Local Similarity: 69.1% Mismatches: 78
Query Match: 68.6% Indels: 3
DB: 9 Gaps: 2
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US-10-626-126-9 (1-391) x US-10-488-421-7 (1-1170)

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Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATCCAGATACATAAGCAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCTTAGCTAGCTTTTGTATAATGCTAGGAAATGCTTTGTCATTTTAGCTTTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAAACCTTAGACATCGAAGTAGTATATTTTTTCTTAACTTGGCCATCTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTTTGTGGTGATCTCCATTCCTTTGTATATCCCTCACAGCTGTCGATGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAATCTGTGTAATTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTTCTCTCATCATGATCGATACCTGTCAGTCTCAAAATGCTGTG 360
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Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCATTATAGAACTCAACATACCTGGGCTCTCAAGATTCTTACTCTGATGGTGGCGGTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCCCTCTTAGTGAAATGGCCCAATGATCTAGTTTCAGAGTCTTGGAGGATGAA 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTCGGAATGGTACATCTCTTGCATCACA 534
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATTCTTGGAAATTCGTGATCCCAAGTCACTCTAGTCGCTTATTTCACATCAATATTAT 594
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGCCAAGCCATCTCTGGACTGCT 654
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAACTCTCTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAAATTCCTGCATCTCTTCAVTCAGAGAGACAGAGAGAGAGTAGT 774
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 775 CTCAATGTTTTCTCAAGAACAGATGAATAGCAATCAATTCCTCAAAATGGGTTC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATCTCTAGCTCTTCCACCAAGGGAACATGTTGAACCTCTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTCTGGCTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTGTTCACAAATGTCCTTCAATTTATTTCTCAGAACACAGGTCTCTAAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1015 TGGTATAGAAATTCGATTTGGCTTCAGTGGTTCATTTCTTTTGTCAATCTCTTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1075 CCATTGTGTCAAGCGCTTCAAAAGGCTTCTTGAATAATATTTTGTATAAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTTACCATCACAAACAGTCGGTCAATCTCTCT 1170
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RESULT 8

US-09-812-216-1

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; Sequence 1, Application US/09812216
; Patent No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monmsa, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
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; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-812-216-1
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Alignment Scores:
Pred. No.: 5,7e-145 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.3% Conservative: 40
Best Local Similarity: 69.1% Mismatches: 78
Query Match: 68.6% Indels: 3
DB: 3 Gaps: 2
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US-10-626-126-9 (1-391) x US-09-812-216-1 (1-1173)

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Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACATAATAGCACAATCAATTTATCATCACTAAGCACTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCTTGTAGCTTTTGTCTAATAGCTAGGAAATGCTTTGTTCATTTAGCTTTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACCTTGGCCATCTCT 180
Qy 61 AspPheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTTGTGGGTGTGATCTCCATTCCTTTGTATCATCTCCACACGCTGTCGAATGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTGGGAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTCCTCTCATCAGTATGATACCTGTCAGTCTCAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCATTATAGAACTCAACATACCTGGGCTCTCAAGATTGTTACTCTGATGGTGGCGGTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCCCTCTTAGTGAAATGGCCCAATGATTCATGTTTCAGAGTCTTGGAGGATGAA 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTCGGAATGGTACATCTCTTGCATCACA 534
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATTCTTGGAAATTCGTGATCCCAAGTCACTCTAGTCGCTTATTTCACATCAATATTAT 594
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGCCAAGCCATCTCTGGACTGCT 654
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAACTCTCTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAAATTCCTGCATCTCTTCAVTCAGAGAGACAGAGAGAGAGTAGT 774
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
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Db 775 CTCAATGTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGGGTTC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACCAAGGGAAACATGTTGAACCTGTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGAGATTAGCAAGTCACGTGGCCATCTCTTGGGGTCTTGTCTGTGTCTGGGTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTGTGTCAAAATGCTCTTCAATTTATTTCTCAGCAACAGGTCTCTAAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 360
Db 1015 TGGTATAGAAATTCGATTTTGGCTTCAGTGGTTCAAATTCCTTCTCAATCAGTT 1074
Qy 361 ProLeuCysHisArgGluSerLeuAlaPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 380
Db 1075 CCATTGTGTCAAGGCTTTCAAGGCTTTCTTGAATAATTTTGTATATAAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCACACACAGTCGGTCAGTATCTTCT 1170

RESULT 9

US-09-910-411-1
; Sequence 1, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derek
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiaotong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70555-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-910-411-1

Alignment Scores:
Pred. No.: 5,7e-145 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.3% Conservative: 40
Best Local Similarity: 69.1% Mismatches: 78
Query Match: 68.6% Indels: 3
DB: 2 Gaps: 2

US-10-626-126-9 (1-391) x US-09-910-411-1 (1-1173)

Qy 1 MetSerGluSerHsGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATCCAGATACATAAGCAATCAATTTATCATCTAAGCACTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTTATGTCTTAGTAGCTTTTGTCTATATAAGTCTTGGTTCATTTTAGCTTTT 120

Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAAAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACCTGGCACTCTCT 180
Qy 61 AppPheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTTGTGGGTGTGATCTCCATTCCTTGTGTATCATCCCTCACAGCTGTTCGAATGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAATCTGTATTTTGGCTCACTACTGACTATCTGTGTGTACAGCA 300
Qy 101 SerValTyrSerIleValLeuLeuSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTCCTCATCAGCTATGATCGATACCTGTGACGTCTCAAAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGAACTCAACATACCTGGGCTTTGAAGATTGTACTCTGATGGTGGCCGTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCCCTTCTTAGTGAATGGGCCAATGATCTTAGTTTCAGAGTCTTGGAGAGATGA 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCCTTGCATCACA 534
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATTCTTGGAAATTCGTATCCAGTCATCTTAGTCGCTTATTTCACATGAATATTTAT 594
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGAAGCGTGATCATCTCAGTAGTGTCCAAAGCCATCCTCGGACGTAGTCT 654
Qy 221 ThrSerArgGlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCT 714
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProHsArgLysSerSer 260
Db 715 TCTGCATCGACAGAAGTTCCTGCATCCTTTCATTCAGAGAGACAGAGGAGAGTAGT 774
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 775 CTCATGTTTCTCAAGAACCAAGATGAATAGCAATACAACTGCTTCCAAAATGGGTTC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCAAAGGGAAACATGTTGAACCTGTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCAAGTCACGTGGCCATCTCTTAGGGGTCTTGTCTGTCTGGGTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTGTGTCAAAATGCTCTTCAATTTATTTCTCAGCAACAGGTCTCTAAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 360
Db 1015 TGGTATAGAAATTCGATTTTGGCTTCAGTGGTTCAAATTCCTTCTCAATCAGTT 1074
Qy 361 ProLeuCysHisArgGluSerLeuAlaPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 380
Db 1075 CCATTGTGTCAAGGCTTTCAAGGCTTTCTTGAATAATTTTGTATATAAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCACACACAGTCGGTCAGTATCTTCT 1170

RESULT 10

US-09-875-076-13
 ; Sequence 13, Application US/09875076
 ; Publication No. US20030017528A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Ruoping
 ; APPLICANT: Dang, Huang T.
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lin, I-Lin
 ; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors

FILE REFERENCE: AREN0050
 ; CURRENT APPLICATION NUMBER: US/09/875,076
 ; CURRENT FILING DATE: 2001-06-06
 ; PRIOR APPLICATION NUMBER: 09/417,044
 ; PRIOR FILING DATE: 1999-10-12
 ; PRIOR APPLICATION NUMBER: 60/120,416
 ; PRIOR FILING DATE: 1999-02-16
 ; PRIOR APPLICATION NUMBER: 60/121,851
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: 60/123,946
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,949
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/136,436
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,437
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/137,127
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/137,131
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/141,448
 ; PRIOR FILING DATE: 1999-06-29
 ; PRIOR APPLICATION NUMBER: 60/156,653
 ; PRIOR FILING DATE: 1999-09-29
 ; PRIOR APPLICATION NUMBER: 60/156,633
 ; PRIOR FILING DATE: 1999-09-29
 ; PRIOR APPLICATION NUMBER: 60/156,555
 ; PRIOR FILING DATE: 1999-09-29
 ; PRIOR APPLICATION NUMBER: 60/157,294
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 60/157,280
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 60/157,293
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 60/157,282
 ; PRIOR FILING DATE: 1999-10-01
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 1173
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-875-076-13

Alignment Scores:
 Pred. No.: 5,7e-145 Length: 1173
 Score: 1403.50 Matches: 271
 Percent Similarity: 79.3% Conservative: 40
 Best Local Similarity: 69.1% Mismatches: 78
 Query Match: 68.6% Indels: 3
 DB: 3 Gaps: 2

US-10-626-126-9 (1-391) x US-09-875-076-13 (1-1173)

Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20

Db	1	ATGCCAGATCTACTATAGCACACATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT	60
Qy	21	LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValAlaIleLeuAlaPhe	40
Db	61	TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCATTTTACGCTTT	120
Qy	41	ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer	60
Db	121	GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACCTGGCCATCTCT	180
Qy	61	AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr	80
Db	181	GACTTCTTTTGGGTGTGATCTCATCTTCTTTGTACATCCCTCAACGCTTTTGAATGG	240
Qy	81	AsnProGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCysThrAla	100
Db	241	GATTTTGGAAAGGAATCTGTGATTATTTGGCTCACTACTGACTATCTGTTATGTACAGCA	300
Qy	101	SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal	120
Db	301	TCTGTATATAACATTTGCTCATCAGCTATGATCGATACCTGTCAGTCTCAAAATGCTGTG	360
Qy	121	ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr	140
Db	361	TCATTAGAACTCAACATCTGGGTCTTGAAGATTGTTACTCTGATGGTGGCGTTTGG	420
Qy	141	IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer	160
Db	421	GTGCTGCCCTTCTTAGTGAATGGCCAATGATCTAGTCTCAGAGTCTTGAAGGATGAA	480
Qy	161	ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrIleLeuAlaIleThr	180
Db	481	GGTAGT-----GAATGTGAACCTGGATTTTTTTCGAATGGTACATCCTTGCATCACA	534
Qy	181	AlaPheLeuGluPheLeuLeuProValSerLeuValTyrPheSerValGlnIleTyr	200
Db	535	TCATTCTTGAATTCTGGATCCAGTCATCTTAGTCGCTATTTCACATGAATATTAT	594
Qy	201	TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla	220
Db	595	TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGCCAAGCCATCTCGAGTACTGCT	654
Qy	221	ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu	240
Db	655	GTCTCTTCCAAACATCTCTGGACACTCATTCAGAGGTAGATATCTTCAAGGAGATCTCT	714
Qy	241	ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer	260
Db	715	CTGCGATCGACAGAAGTTCTGTCATCTTTCATTTCAGAGAGACAGAGGAGAGTAGT	774
Qy	261	LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer	280
Db	775	CTCATGTTTTCCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTCC	834
Qy	281	PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly	300
Db	835	TTCTCCCAATCAGATTCGTAGCTCTTCCAAAGGGAACATGTTGAACCTGCTTAGAGCC	894
Qy	301	ArgLysLeuAlaArgSerLeuAlaValLeuSerAlaPheAlaIleCysTyrAlaPro	320
Db	895	AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGGTTTTTGTCTTGTCTGGGTCCA	954
Qy	321	TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle	340
Db	955	TATTCCTGTTTCAATTTGCTCTTTCATTTTATTCCTCAGCAACAGTCTCTAATCAGTT	1014
Qy	341	TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr	360
Db	1015	TGGTATAGAATTGCAITTTGGCTTCAGTGGTTCATTTCTCTTGTCAATCTCTCTTTGTAT	1074
Qy	361	ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln	380


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Db 655 GTCTCTTCCACATCTGTGGACATCATTCAGAGGTAGACTATCTTCAAGAGATCTCTT 714
Qy 241 ProGlyLeuYsGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAAAGTTCCTGCATCTCTTCAATTCAGAGACAGAGAGAGAGTAGT 774
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerLeuLeuAlaPheLysValGlySer 280
Db 775 CTCTATGTTTCTCAAGAACCAAGATGAATAGCAATCAATTTGCTTCCAAATGGGTCC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCATCAGATCTGTAGCTCTTCACCAAGGGACATGTTGAATGCTTAGAGCC 894
Qy 301 ArgYsLeuAlaAlaSerLeuAlaValLeuLeuSerAlaPheAlaLeuCysTrpAlaPro 320
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGGTTTTGCTTGTGGGTCCA 954
Qy 321 TyrCysLeuPheThrLeuValLeuSerThrTyrArgArgGlyGluArgProLysSerLe 340
Db 955 TATTCTCTGTTTCAAAATGCTCTTTTCAATTTTATTTCTCAGCAACAGGTCTTAAATCAGT 1014
Qy 341 TrpTyrSerLeuAlaPheTrpLeuGlnTrpPheAsnSerLeuLeuAsnProPheLeuTyr 360
Db 1015 TGGTATAGAAATGCAATTTGGCTTCAGTGGTTCATTTCTTGTCAATCTCTTTGTAT 1074
Qy 361 ProLeuYsHisArgGlyPheGlnLysAlaPheTrpLysLeuLeuCysValTrpLysGln 380
Db 1075 CCATTTGTGCACAGCGCTTCAAAAGCGTTCTTGAATAATATTTGTATAAAAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTTACCATCACACACAGTCGGTCAATCTCTTCT 1170
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RESULT 12

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US-10-052-193-1
; Sequence 1, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052.193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-193-1
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Alignment Scores:
Pred. No.: 5.7e-145 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.3% Conservative: 40
Best Local Similarity: 69.1% Mismatches: 78
Query Match: 68.6% Indels: 3
DB: 5 Gaps: 2
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US-10-626-126-9 (1-391) x US-10-052-193-1 (1-1173)

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Qy 1 MetSerGluSerAnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaLeuThrLeuGlyLeuAlaValAlaValLeuAlaPhe 40
Db 61 TTTATGCTCTTAGTACCTTTTGCTATATGCTAGGAATGCTTTGGTCAATTTTAGCTTTT 120
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RESULT 13

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Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaLeuSer 60
Db 121 GTGTGTGCAAAACCTTAGACATCGAAGTAGTATATTTTTTTTCTTAACCTTGCCATCTCT 180
Qy 61 AspPhePheValGlyValLeuSerLeuProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTCTTTTGGGTGTGATCTCCATTTCTTTGTATCATCCCTCACACGCTGTCGAATGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAATCTGTATATTTTGGCTCACTACTGACTATCTGTATGTATGACGCA 300
Qy 101 SerValTyrSerLeuValLeuLeuSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATACATTTGCTCTCATCAGTATGATCGATACCTGTCAAGTCTCAATAGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTATAGAACTCAACATCACTGGGTCTTGAAGATTGTTACTCTGATGGTGGCGTTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGGAAGGATGAA 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTTGGCCATCACA 534
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATTTCTGGAAATTCGTGATCCCGATCATCTTAGTCGCTTATTTCAACATGAATATTTAT 594
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGCCAAAGCCATCTCTGGACTGACTGCT 654
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAAACATCTGTGACATCTCAATTCAGAGGTAGACTATCTTCAAGAGATCTCTT 714
Qy 241 ProGlyLeuYsGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAGTTCCTGCATCTCTTCAATTCAGAGACAGAGAGAGAGTAGT 774
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerLeuLeuAlaPheLysValGlySer 280
Db 775 CTCTATGTTTCTCAGAAACCAAGATCAATAGCAATACAATTTGCTTCCAAATGGGTCC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATCTGTAGCTCTTTCACCAAGGGGAACATGTTGAATGCTTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaLeuCysTrpAlaPro 320
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGGTTTTGCTGTTTGGTGGGTCCA 954
Qy 321 TyrCysLeuPheThrLeuValLeuSerThrTyrArgArgGlyGluArgProLysSerLe 340
Db 955 TATTCTCTGTTTCAAAATGCTCTTTTCAATTTTATTTCTCAGCAACAGGTCTTAAATCAGT 1014
Qy 341 TrpTyrSerLeuAlaPheTrpLeuGlnTrpPheAsnSerLeuLeuAsnProPheLeuTyr 360
Db 1015 TGGTATAGAAATGCAATTTGGCTTCAGTGGTTCATTTCTTGTCAATCTCTTTGTAT 1074
Qy 361 ProLeuYsHisArgGlyPheGlnLysAlaPheTrpLysIleLeuCysValTrpLysGln 380
Db 1075 CCATTTGTGCACAGCGCTTCAAAAGCGTTCTTGAATAATATTTGTATAAAAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTTACCATCACACACAGTCGGTCAATCTCTTCT 1170
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US-10-272-983-13		
; Sequence 13, Application US/10272983		
; Publication No. US20030148450A1		
; GENERAL INFORMATION:		
; APPLICANT: Chen, Ruoping		
; APPLICANT: Dang, Huong T.		
; APPLICANT: Liaw, Chen W.		
; APPLICANT: Lin, I-Lin		
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors		
; FILE REFERENCE: AREN0050		
; CURRENT APPLICATION NUMBER: US/10/272,983		
; CURRENT FILING DATE: 2002-10-17		
; PRIOR APPLICATION NUMBER: US/09/417,044		
; PRIOR FILING DATE: 1999-10-12		
; PRIOR APPLICATION NUMBER: 60/109,213		
; PRIOR FILING DATE: 1998-11-20		
; PRIOR APPLICATION NUMBER: 60/120,416		
; PRIOR FILING DATE: 1999-02-16		
; PRIOR APPLICATION NUMBER: 60/121,851		
; PRIOR FILING DATE: 1999-02-26		
; PRIOR APPLICATION NUMBER: 60/123,946		
; PRIOR FILING DATE: 1999-03-12		
; PRIOR APPLICATION NUMBER: 60/123,949		
; PRIOR FILING DATE: 1999-03-12		
; PRIOR APPLICATION NUMBER: 60/136,436		
; PRIOR FILING DATE: 1999-05-28		
; PRIOR APPLICATION NUMBER: 60/136,437		
; PRIOR FILING DATE: 1999-05-28		
; PRIOR APPLICATION NUMBER: 60/136,439		
; PRIOR FILING DATE: 1999-05-28		
; PRIOR APPLICATION NUMBER: 60/136,567		
; PRIOR FILING DATE: 1999-05-28		
; Remaining Prior Application data removed - See File Wrapper or PALM.		
; NUMBER OF SEQ ID NOS: 74		
; SOFTWARE: PatentIn Ver. 2.1		
; SEQ ID NO 13		
; LENGTH: 1173		
; TYPE: DNA		
; ORGANISM: Homo sapiens		
US-10-272-983-13		
Alignment Scores:		
Pred. No.:	5.7e-145	Length: 1173
Score:	1403.50	Matches: 271
Percent Similarity:	79.3%	Conservative: 40
Best Local Similarity:	69.1%	Mismatches: 78
Query Match:	68.6%	Indels: 3
DB:	6	Gaps: 2
US-10-626-126-9 (1-391) x US-10-272-983-13 (1-1173)		
Qy	1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20	
Db	1 ATGCCAGATACCTAATGACCAATCAATTTTATCACTAAGCACTCGTGTACTTTAGCATTT 60	
Qy	21 LeuMetSerLeuAlaPheAlaThrIleGlyAsnAlaValValIleLeuAlaPhe 40	
Db	61 TTTATGCTCTAGTACCTTTGCTAATAGCTAGGAATGCTTTGTCATTTAGCTTTT 120	
Qy	41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60	
Db	121 GTGTGGACAAAACCTAGACATCGAAGTAGTATTTTCTTAACCTTGGCCATCTCT 180	
Qy	61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80	
Db	181 GACTTCTTTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTCGAATGG 240	
Qy	81 AsnProGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeuLeuCysThrAla 100	
Db	241 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300	
Qy	101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120	

US-10-354-769-1
; Sequence 1, Application US/10354769
; Publication No. US20030149242A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: O'Reilly, Mark A.
; APPLICANT: Peter, Beate
; TITLE OF INVENTION: NOVEL POLYPEPTIDE
; FILE REFERENCE: PC10373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243

RESULT 14

Db	301	TCGTATATAACATTTGCTCCTCATGATCGATACCTGTCAGTCTCAATGCTGTG 360
Qy	121	ArgTyrArgAlaGlnHisThrGlyIleLeuValIleValAlaGlnMetValAlaValTyr 140
Db	361	TCCTTAGAACCTCAACATACCTGGGTCCTTGAAGATTGTTACTCTGATGTGGCGGTTGG 420
Qy	141	IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db	421	GTCTGGCCCTTCTTAGTGAATGGCCCAATGATTTAGTTTTCAGAGTCTTGGAGGATGAA 480
Qy	161	ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTrpTyrIleLeuAlaIleThr 180
Db	481	GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTCTGTCATCACA 534
Qy	181	AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db	535	TCATTTCTTGGAAATTCGTGATCCAGTCATCTTAGTCCTTATTTTCAACATGAATATTTAT 594
Qy	201	TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db	595	TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGTGCCAAAGCCATCTCGACTGCTGCT 654
Qy	221	ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db	655	GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCT 714
Qy	241	ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db	715	TCGCAATCGACAGAGTTCTCTGCATCTCTTCAATTCAGAGAGACAGAGGAGAGAGTAGT 774
Qy	261	LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db	775	CTCATGTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTTC 834
Qy	281	PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db	835	TTCTCCCAATCAGATTTCTGTAGCTCTTCCACAAAGGGAACATGTTGAACCTTAGAGCC 894
Qy	301	ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db	895	AGGAGATTAGCCAAAGTCACCTGGCCATCTCTTAGGGGTTTTGCTGTTTGGTGGGTCCA 954
Qy	321	TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db	955	TATTCCTCTGTTCACAATTTGCTTTTCATTTTATCTCAGCAACAGCTCTCTAAATCAGTT 1014
Qy	341	TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuLeuAsnProPheLeuTyr 360
Db	1015	TGGTATAGAAATTCGATTTTGGCTTCAGTGGTTCAATTCCTTTGCTCAATCCTCTTTGTAT 1074
Qy	361	ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db	1075	CCATTGTGTACAGCGCTTTCAAAAGGCTTTCTTGAANAATATTTTGTATAAAAAGCAA 1134
Qy	381	ProAlaProSerGln---ThrGlnSerValSerSer 391
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; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-354-769-1

Alignment Scores:
Pred. No.:      5.7e-145      Length:      1173
Score:          1403.50      Matches:      271
Percent Similarity: 79.3%      Conservative: 40
Best Local Similarity: 69.1%      Mismatches: 78
Query Match:      68.6%      Indels:      3
DB:               6          Gaps:      2

US-10-626-126-9 (1-391) x US-10-354-769-1 (1-1173)

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Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTTATGTCTCTAGTAGCTTTTGTCTATAATGCTAGGAATGCTTTGGTCAATTTAGCTTTT 120

Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGTGGACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTTGGCCATCTCT 180

Qy 61 AspPheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80
Db 181 GACTCTTTGGGTGGTGAATCTCAATTCCTTTGTACATCCTTCACGCGTTCGAATGG 240

Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAATCTGTGTATTTTGGTCACTACTGACTATCTGTTATGTACAGCA 300

Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATGTCTCATCAGCTATGATCAGTACCTGTGTCAGTCTCAAAATGCTGTG 360

Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGAACTCAACATCTGGGTCTTGAAGATTGTTACTCTGATGGTGGCCGTTGG 420

Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCCCTTCTAGTGAATGGSCCAATGATTCCTAGTCTCAGAGTCTTGGAGGATGAA 480

Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrPheIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTCTTGGCCATCACA 534

Qy 181 AlaPheLeuGluPheLeuProValSerLeuValTyrPheSerValGlnIleTyr 200
Db 535 TCATCTTGTGAATTCGTGATCCCAAGTCACTCTTAGTCGCTTATTTCAACATGAATATTAT 594

Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGGAGCTGATCATCTCAGTAGTGGCCAAAGCCATCTCTGAGCTGACTGCT 654

Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAACATCTGTGGACACTCATCTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714

Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAGTTCTCTGCATCTCTTTCATTCAGAGAGACAGAGAAAGAGTAGT 774

Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
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Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
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Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGGTTTTTGTCTGTTGGTGGCTCCA 954

Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTCTGTTCACAAATTTGCTTTTCATTTTATTTTCTCAGCAACAGGTCCTAAATCAGTT 1014

Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
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Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
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Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
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RESULT 15
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; Sequence 13, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-393-807-13

Alignment Scores:
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GenCore version 5.1.7
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Run on: April 29, 2006, 02:01:23 ; Search time 5383 Seconds
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294.995 Million cell updates/sec

Title: US-10-626-126-9

Perfect score: 2045

Sequence: 1 MSESNGTDVLPFTAQVPLAP.....WKILCVTKQAPAPSTQSVSS 391

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Ygapop 10.0	Ygapext 0.5	
Rgapop 6.0	Rgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 9295968 seqs, 2030634719 residues

Total number of hits satisfying chosen parameters: 18591936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DALIGN=200 -THR_SCORE=pct -THR_MAX=100
-MAXLEN=2000000000 -HOST=abs803p
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Database : Published Applications NA New:

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15:	/SID55/ptodata/2/pubpna/US60 NEW PUB seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	682	33.3	2761	11 US-11-036-196-2003 Sequence 2003, Ap
2	682	33.3	2814	14 US-11-136-527-3990 Sequence 3990, Ap

3	621	30.4	2824	14	US-11-136-527-127	Sequence 127, App
4	594	29.0	1326	14	US-11-241-956-19	Sequence 19, Appl
5	407.5	19.9	2348	14	US-11-136-527-3691	Sequence 3691, Ap
6	405	19.8	1773	14	US-11-127-877-17	Sequence 17, Appl
7	405	19.8	1974	14	US-11-124-368A-14	Sequence 14, Appl
8	401	19.6	2733	14	US-11-136-527-2435	Sequence 2435, Ap
9	400.5	19.6	4095	14	US-11-136-527-2030	Sequence 2030, Ap
10	400	19.6	2699	14	US-11-127-877-5	Sequence 5, Appl
11	399.5	19.5	3578	11	US-11-036-196-1495	Sequence 1495, Ap
12	392	19.2	2633	14	US-11-136-527-3114	Sequence 3114, Ap
13	387.5	18.9	1860	14	US-11-136-527-2642	Sequence 2642, Ap
14	376.5	18.4	3741	14	US-11-136-527-751	Sequence 751, App
15	374.5	18.3	4061	14	US-11-136-527-2806	Sequence 2806, Ap
16	372.5	18.2	2089	14	US-11-128-061-892	Sequence 892, App
17	372.5	18.2	2089	14	US-11-128-049-892	Sequence 892, App
18	370.5	18.1	1303	14	US-11-128-061-570	Sequence 570, App
19	370.5	18.1	1303	14	US-11-128-049-570	Sequence 570, App
20	365.5	17.9	2089	14	US-11-127-877-14	Sequence 14, Appl
21	365.5	17.9	2290	14	US-11-127-877-13	Sequence 13, Appl
22	361	17.7	1401	14	US-11-127-877-4	Sequence 4, Appl
23	359	17.6	85980	11	US-11-114-798-46	Sequence 46, Appl
24	359	17.6	197241	11	US-11-114-798-47	Sequence 47, Appl
25	357.5	17.5	1496	14	US-11-136-527-2608	Sequence 2608, Ap
26	356.5	17.4	1443	8	US-10-521-162-39	Sequence 39, Appl
27	356.5	17.4	1443	8	US-10-521-162-41	Sequence 41, Appl
28	353	17.3	2591	14	US-11-136-527-1944	Sequence 1944, Ap
29	352.5	17.2	1203	9	US-10-499-210-1	Sequence 1, Appl
30	349.5	17.1	2483	14	US-11-136-527-2847	Sequence 2847, Ap
31	349.5	17.1	2509	14	US-11-136-527-3738	Sequence 3738, Ap
32	341.5	16.7	1435	8	US-10-750-185-26145	Sequence 26145, A
33	341.5	16.7	1435	8	US-10-750-623-26145	Sequence 26145, A
34	339.5	16.6	3893	14	US-11-136-527-2295	Sequence 2295, Ap
35	337.5	16.5	1350	11	US-11-232-805-24	Sequence 24, Appl
36	337.5	16.5	1862	14	US-11-136-527-2377	Sequence 2377, Ap
37	337.5	16.5	2809	14	US-11-136-527-2036	Sequence 2036, Ap
38	336.5	16.5	1350	11	US-11-232-805-25	Sequence 25, Appl
39	333.5	16.3	1552	14	US-11-136-527-2107	Sequence 2107, Ap
40	329	16.1	1344	11	US-11-232-805-2	Sequence 2, Appl
41	328.5	16.1	1353	11	US-11-232-805-1	Sequence 1, Appl
42	328.5	16.1	6501	14	US-11-136-527-3427	Sequence 3427, Ap
43	315.5	15.4	1269	14	US-11-136-527-3749	Sequence 3749, Ap
44	311.5	15.2	5616	14	US-11-136-527-2020	Sequence 2020, Ap
45	303	14.8	6244	14	US-11-136-527-3243	Sequence 3243, Ap

ALIGNMENTS

RESULT 1
US-11-036-196-2003
; Sequence 2003, Application US/11036196
; Publication No. US20060078900A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgins, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/11/036,196
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US/10/152,319
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807

;; PRIOR FILING DATE: 2001-07-10
;; PRIOR APPLICATION NUMBER: US 60/303,808
;; PRIOR FILING DATE: 2001-07-10
;; PRIOR APPLICATION NUMBER: US 60/315,047
;; PRIOR FILING DATE: 2001-08-28
;; PRIOR APPLICATION NUMBER: US 60/324,928
;; PRIOR FILING DATE: 2001-09-27
;; PRIOR APPLICATION NUMBER: US 60/330,867
;; PRIOR FILING DATE: 2001-11-01
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 2221
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2003
;; LENGTH: 2761
;; TYPE: DNA
;; ORGANISM: Rattus norvegicus
;; FEATURE:
;; OTHER INFORMATION: Genbank Accession No. NM_053506
US-11-036-196-2003

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Query Match: 33.3% Indels: 88
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US-10-626-126-9 (1-391) x US-11-036-196-2003 (1-2761)

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Qy 38 LeuAlaPheValAlaPheArgAsnLeuArgHiAArgSerAsnTyrPhePheLeuAsnLeu 57
Db 506 CTGGCTCTGTCGGCGATTCCAGCCTCCGCCACAGAACCACTTTCTTCTGCTCAACCTC 565

Qy 58 AlaIleSerAspPhePheValGlyValIleSerIlePheLeuProLeuTyrIleProHisThrLeu 77
Db 566 GCATCTCCGACTTCTCTGCGGGTGCCTTCGTATCCCATGTCAGTACCCCTATGTCGTG 625

Qy 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 626 ACCGGCGGTGGACCTTCGGCGGGGCTCTGCAAGCTGGCTGGTGGTAGACTACCTA 685

Qy 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 686 CTGTGTGCTCTCTCGGTCTTCAACATCGTACTCATCAGCTATGACCGATTCTGTGTCAGTC 745

Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMet 136
Db 746 ACTCGAGCTGTCTTACAGGGGCCACAGGGGACACAGAGCGGGCGGTTCGGAAGATG 805

Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 806 GCATGTGTGGTGTGGCTCTCTCTGCTATGGGCTGCCATCTG-----AGT 856

Qy 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 857 TGGGAGTACCTGTGTGGTGCAGTTCCATCCCGAGGGCCACTGCTATGCTGAGTTCTTC 916

Qy 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
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Db 1097 GCTCCCCCAGCTGCTGGGCTGCTGGCCAAAGGCGCATGGCGAGCCATGCCGTTGCAC 1156

Qy 216 AlaGlyPheIleAlaThrSerSerArgGlyThr-----Gly 227
Db 1157 AGGTATGGGTGGTGCAGGCGCCCTGGTGTGGAGCTGGGAGGCTGCCCTCGGGGT 1216

Qy 228 HisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeuLysGluProAla 247
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Qy 268 HisMetSerGlySerIleIleAlaPheLysValGlySerPheCysArgSerGluSerPro 287
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Qy 288 ValLeuHisGlnArg-----GluHisValGluLeuLeu 298
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Qy 299 ArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrp 318
Db 1391 CGGACACAGAGGTGGCCAAAGTCGCTGGCCATCATCGTGAGCATCTTTGGGCTCTGCTGG 1450

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Qy 339 SerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPhe 358
Db 1508 GATTACTGGTACGAGCGCTTCTGGCTTCTGTGGGCCAACTCGGCCGTCGCAACCCGTC 1567

Qy 359 LeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThr 378
Db 1568 CTCTACCCACTGTGCCACTACAGCTTCGCGAGAGCCTTCACCAAGCTCTCTGCCCCCAG 1627

Qy 379 Lys-----GlnProAlaProSerGlnThrGln 387
Db 1628 AAGCTCAAGTCCAGGCCCAAGCGCTCCCTGGAGCAG 1663

RESULT 2
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; Sequence 3990, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AMI01086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3990
; LENGTH: 2814
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3990

Alignment Scores:
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Score: 682.00 Matches: 160
Percent Similarity: 48.8% Conservative: 51
Best Local Similarity: 37.0% Mismatches: 133
Query Match: 33.3% Indels: 88
DB: 14 Gaps: 10

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Db 436 CTGGCTGGCTCATGGCGCTGCTCATGTGGCCACAGTACTGGGCAACGGCGTGGTCATG 495
Qy 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 496 CTCGCCCTCGTGGCGGATTCGAGGCTCCGACCCAGAACAACTCTTTCTGCTCAACCTC 555
Qy 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuFyrIleProHisThrLeu 77
Db 556 GCCATCTCCGACTCTCTCGTGGTGGCTTCGCAATCCCATTTGATGAGTACCTATGTGCTG 615
Qy 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 616 ACCGGCGCTTGGACCTTCGGCGCGGCTCTGCAAGCTGTGGCTGGTGGTAGACTACTA 675
Qy 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 676 CTGTGTGCCCTCTCGGCTTCAACATCGTACTCATCAGCTATGACGATTCCTGTCAGTC 735
Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMet 136
Db 736 ACTCAGCTGTCTCTACAGGCGCCAGCAGGGGACAGAGACGGCGGTTCGGAAGATG 795
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 796 GCACGTGTGGTGGTGGCTCTCTGCTGATGGGCTGCATCTCTG-----AGT 846
Qy 157 TrpIys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 847 TGGGAGTACCTGTCTGTGGTGGAGTTCCATCCCGAGGGCCACTGCTATGTGATTTCTTC 906
Qy 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
Db 907 TACACTGGTGTACTTTCATCAGCGCTTCCACCCCTCGAGTTCTTCAGCCCTTCTCAGC 966
Qy 192 ValValTyrPheSerValGlnIleTyr----- 200
Db 967 GTTACCTTCTCAACCTCAGCATCTACCTGAACATCCAGAGCGCACCCGCTTCGGCTT 1026
Qy 200 ----- 200
Db 1027 GATGGGGCGCTGAGGCTGGCCCAAGACCCCCACACAGATGCCAGCCCTGCCACCTCCA 1086
Qy 201 -----TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHis 215
Db 1087 GTTCCCCCAGCTGCTGGGGCTGTGGCCAAAGGGCATGGCGAGGCCATGGCGTTGCAC 1146
Qy 216 AlaGlyPheIleAlaThrSerSerArgGlyThr-----Gly 227
Db 1147 AGGTATGGGTGGTGGAGCGGCGCTGTGTGAGCTGGGAGGGCTGGCCCTCGGGGT 1206
Qy 228 HisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeuLysGluProAla 247
Db 1207 GGCAGTGGTGGAGTGTGCTGCTCCCTCCACCTCCAGCTCCAGCTCTGCG-----AGC 1254
Qy 248 AlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuLeuValSerLeuArgThr 267
Db 1255 TCCTCAAGGGGCACTGAGAGGCCACGC----- 1281
Qy 268 HisMetSerGlySerIleAlaPheLysValGlySerPheCysArgSerGluSerPro 287
Db 1282 -----TCACTCAAAGGGGCTCCAGGCATCAGCATCTTCAGCA 1320
Qy 288 ValLeuHisGlnArg-----GluHisValGluLeuLeu 298
Db 1321 TCCCTGAGAAGCGCATGAAGATGGTGTCCAGAGCATCACCCAGCGCTTCGCGCTGTGC 1380
Qy 299 ArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrp 318
Db 1381 CCGGACAAGAGGTGGCCAAAGTCCGTGGCCATCATCGTGGCATCTTTGGGCTCTGCTGG 1440
Qy 319 AlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLys 338
Db 1441 GCGCGGTACACGGCTCTCTAATGATCATCCGAGCTGCTTGC---CATGGCCGCTGCATCCCC 1497
Qy 339 SerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPhe 358
Db 1498 GATTACTGGTACGAGAGCTCTTCTGCTTCTGTGGGCCAACTGGCGGTCAACCCGTC 1557
Qy 359 LeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeuCysValThr 378
Db 1558 CTCTACCCACTGTGCCACTACAGCTTCGCGAGAGCCTTCACCAAGCTCTCTGCCCCCAG 1617
Qy 379 Lys-----GlnProAlaProSerGlnThrGln 387
Db 1618 AAGCTCAAGGTCCAGCCCCCAGCGCTCCTCGAGCAG 1653
RESULT 3
US-11-136-527-127
; Sequence 127, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AMI101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127
; LENGTH: 2824
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-127
Alignment Scores:
Pred. No.: 3,61e-45 Length: 2824
Score: 621.00 Matches: 151
Percent Similarity: 46.1% Conservative: 48
Best Local Similarity: 35.0% Mismatches: 145
Query Match: 30.4% Indels: 88
DB: 14 Gaps: 10
US-10-626-126-9 (1-391) x US-11-136-527-127 (1-2824)
Qy 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAenAlaValValle 37
Db 446 CTGGCTGGCTCATGGCGCTGCTCATGTGGCCACAGTACTGGGCAACGGCGTGGTCATG 505
Qy 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 506 CTCGCCCTCTGTGGCGGATTCGAGGCTCCGACCCAGAACAACTCTTTCTGCTCAACCTC 565
Qy 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuFyrIleProHisThrLeu 77
Db 566 RSKAKTCSGACWKSSTGCTGGGTGGCTTCTGTCATCCATTTGATGACCTATGTCGTG 625
Qy 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 626 ACCGGCGCTTGGACCTTCGGCGCGGCTCTGCAAGCTGTGGCTGGTGGTAGACTACTA 685
Qy 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 686 CTGTGTGCCCTCTCGGCTTCAACATCGTACTCATCAGCTATCAGCATTCCTGTCAGTC 745
Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMet 136
Db 746 ACTCGAGTGTCTCTTACAGGGGCCACAGAGCGGGGACACAGAGCGGCGCTTCGGAAGATG 805
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Qy	139	V	AltpPleLeuA	PheLeuVal	AeNglyProMetIleLeuA	SerAspSerTrpLys	158
Db	574	G	TTTTGGGTCGTGGCCCTTCTAGTAGTAATGGGCCAAATGAATTCTAGTTTTCAGAGTCTTTGGGAG				633
Qy	159	A	nSerThrAnThrGlUgluCysGluProGlyPheValThrGluTrpTyrlleLeuA				178
Db	634	G	ATGNAAGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAAATGGTGACATCTTGGC				687
Qy	179	I	lThralaPheLeuGluPheLeuLeuProValSerLeuValValTyrrPheSerValGln				198
Db	688	A	TCAATCATCTTGGAAATTCGTGTATCCAGTGCATCTTAGTCGCTATTATTTCAACATGAAT				747
Qy	199	I	leTyrrTrpSerLeuTrpLysArgGlySerLeu				209
Db	748	A	TTTTATTGGAGCCTGTGGAAGCGTGATCATCTC				780
RESULT 5							
US-11-136-527-3691							
; Sequence 3691, Application US/11136527							
; Publication No. US20050287570A1							
; GENERAL INFORMATION:							
; APPLICANT: Wyeth							
; APPLICANT: Mounts, William M							
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes							
; FILE REFERENCE: 031898-041000 (AM101086)							
; CURRENT APPLICATION NUMBER: US/11/136,527							
; CURRENT FILING DATE: 2005-05-25							
; PRIOR APPLICATION NUMBER: US 60/574,294							
; PRIOR FILING DATE: 2005-05-26							
; NUMBER OF SEQ ID NOS: 362830							
; SOFTWARE: PatentIn version 3.2							
; SEQ ID NO 3691							
; LENGTH: 2348							
; TYPE: DNA							
; ORGANISM: Rattus norvegicus							
US-11-136-527-3691							
Alignment Scores:							
Pred. No.: 3.92e-26 Length: 2348							
Score: 407.50 Matches: 136							
Percent Similarity: 40.2% Conservative: 79							
Best Local Similarity: 25.4% Mismatches: 166							
Query Match: 19.9% Indels: 155							
DB: 14 Gaps: 18							
US-10-626-126-9 (11-391) x US-11-136-527-3691 (1-2348)							
Qy	4	SerAeNglyThrAspValLeuProLeuThrAlaGln-----ValProLeu	18				
Db	282	TCAAACGACACACTCCAGCACCCCTCGGGGGTCACACCATCTGGCAAGTCGTCTTCATT	341				
Qy	19	AlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValllleu	38				
Db	342	GCCTTCTTAACCGGCTTCTCGCATVTGTGTGACCATCATCTTGGCAACATCTCTGTGCATTGTG	401				
Qy	39	AlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrrPhePheLeuAsnLeuA	58				
Db	402	GCCTTCAAGGTCAACAACACGCTGAAGACAGTCAACACTACTTCTCTTAAGCTTGCC	461				
Qy	59	IleSerAppPhePheValGlyValllleSerlleProLeuTyrrileProHishThrLeuPhe	78				
Db	462	TGTGCAGACCTGATCATCTCGGGGTCAATTTCCATGAACCTGTTCACCTACATCATCATG	521				
Qy	79	AnS---TrpAnProGlySerGlylleCysMetPheTrpLeulleThrAspTyrrleuLeu	97				
Db	522	AACCGTTGGGCACCTGGGGAACCTAGCCCTGCGACCTCTCGCATTCATGATGATGCGC	581				
Qy	98	CystHalaSerValTyrrSerlleValleulleSerTyrrAspArgTyrrGlnSerValSer	117				
Db	582	AGCAATGGCTTGTGATCAAGAATCTGCTGGTCATCAGCTTGCAGAGTACTTTTCCATCACT	641				
Qy	118	AsnAlaValArgTyrrArgAlaGlnHishThrGlyrlleLeuLyleValalaGlnMetVal	137				

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QY 360 rProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeu-----CysVa 377
Db 1760 TGCCTGTGCAACAACAATTCAGAACCACTTCAGATGCTCTCTGTGGCCAGTGTGA 1819

QY 377 lThryLysGlnProAlaProSerGlnThrGlnSerValSerSer 391
Db 1820 CAAAAGGAGAGGCGCAACAGCAGTACCAAGCAGAGACAGTCG 1862

RESULT 6
US-11-127-877-17
; Sequence 17, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-17

Alignment Scores:
Pred. No.: 4,61e-26 Length: 1773
Score: 405.00 Matches: 141
Percent Similarity: 41.7% Conservative: 83
Best Local Similarity: 26.3% Mismatches: 159
Query Match: 19.8% Indels: 155
DB: 14 Gaps: 19

US-10-626-126-9 (1-391) x US-11-127-877-17 (1-1773)

QY 2 SerGluSerAsnGlyThrAspValLeuProLeuThrAlaGln-----Val 16
Db 148 TCCTCTCCAGACGGTACCAACCGATGACCTCTGGGAGGTCTATCCCGTCTGGCAAGTGGTC 207

QY 17 ProLeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValVal 36
Db 208 TTATCGCTTCTTAAAGGCGATCTGGCCCTTGGTGACCATCATCGGCAACATCTCTGGTA 267

QY 37 IleLeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsn 56
Db 268 ATTGTGTCAATTAAGGTCAACAAGCAGCTGAAGACGGTCAACAACACTTCTCTTAAAGC 327

QY 57 LeuAlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThr 76
Db 328 CTGGCTGTGCCGATCTGATTAATCGGGGTCAATTCATGAATGATCTGTTTACGACCTATAC 387

QY 77 LeuPheAsn---TrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyr 95
Db 388 ATCATGAATCGATGGCGCTTAGGAACCTTGGCTGTGACCTGTGGCTTGGCCATGTACTAC 447

QY 96 LeuLeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSer 115
Db 448 GTAGCCAGCAATGCCCTCTGTTATGAATCTTCGTGTCATCAGCTTTCGACATATCTTTCC 507

QY 116 ValSerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGln 135
Db 508 ATCAGGAGCGCTCAGTACCGAGCAACGAACA-----ACAAAGAGAGCGCGGTGTG 561
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QY 136 MetValAlaVal---TrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSer 154
Db 562 ATGATCGGCTGGCTTGGGTGCATCTCTTGTCTTGGCTCTCCATCCATCTTG----- 615

QY 155 AspSerTrp-----LysAsnSerThrAsnThrGluGluCysGluProGly 169
Db 616 ---TTCTGGCAATACCTTTGTTGGAAGAAGAACTGTGCCCTCCGGGAGAGTGTTCATTTCAG 672

QY 170 PheValThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProVal 189
Db 673 TTCCTCAGTGAGCCCAACCAATTAATTTTGGCAGACCCATCGCTGCTTTTATATGCTGTC 732

QY 190 SerLeuValValTyrPheSerValGln----- 198
Db 733 ACCATTATGAC-TATTTTATCTGGAGGATCTATAAGAGAAACTGAAAAGCGTACCAAGA 791

QY 199 IleTyrTrp-----SerLeuTrpLysArgGly---SerLeuSerArgCysProSerHis 215
Db 792 GCTTGTCTGGCTGCAAGCCTCTGGGACAGAGGAGAGACAGAAAACCTTTGTCCACCCAC 851

QY 216 AlaGlyPheIleAlaThrSerSerArgGlyThrGly----- 227
Db 852 GGGCAGTTCTCGAAGCTGCAGAGTACGAACCTTCAACAGCAAGCATGAAACGCTCCAA 911

QY 228 -----HisSerArgArgThrGlyLeuAlaCys 236
Db 912 CAGGAGGAAGTATGGCGCTGCCACTTCTGTGTTTCAACAACCAAGAGCTGGAACCCAGCTC 971

QY 237 ArgThrSer----- 239
Db 972 CGAGCAGATGGACCAAGACACAGCAGCAGTGTGGAACAACAATGATGCTGCTGC 1031

QY 240 LeuProGly-----LeuLysGluProAlaAla 248
Db 1032 CTCCTGGAGAACTCCGCTCTCCACGAGGAGGACATGGTCCGAGCAGAGAGCCAT 1091

QY 249 SerLeuHisSerGluSerProArgGlyLys-SerSerLeuLeuValSerLeuArgThrHi 268
Db 1092 CTACTCCATCGTGTCTCAAGCTTCGGGTTCACAGCACCACCTCACTCCACCAAGTATCC 1151

QY 268 sMetSerGlySerIle----- 11 274
Db 1152 CTCATCGGACAACTGTCAGGTGCTGAGGAGGAGCTGGGATGGTGGACTTGGAGAGGAA 1211

QY 274 eAlaPheLysVal-----GlySerPheCysArgSer-- 284
Db 1212 AGCCGACAAGCTGTCAGGCCCCAGAGAGCGTGGACGATGGAGGCGAGCTTTCCAAAAGCTT 1271

QY 285 -----GluSerProVal----- 288
Db 1272 CTCCAAGCTTCCCATCCAGCTAGAGTCAGCGTGGACACAGCTAAGACTTCTGACGTCAA 1331

QY 288 ----- 288
Db 1332 CTCCTCAGTGGGTAAAGACGACGCGCCACTCTACCTCTGTCTTCAAGGAAGCCACTCTGGC 1391

QY 289 -----LeuHisGlnArgGluHisValGluLeuLeu 298
Db 1392 CAAGAGGTTTGTCTCGAAGACCAGAGTGCAGTCACTAAGCGGAAGAGATGTCCTCGGT 1451

QY 298 uArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTr 318
Db 1452 CAAGGAGAGAAGAGCGGCCAGACCCCTCAGTGGCATCTTGTGCTTCATCATCATCTTG 1511

QY 318 palAProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLy 338
Db 1512 GACCCCATCAACATCATGTCTCTGTG---AACACCTTTTGTGACAGCTGCATATCCCAA 1568

QY 338 sSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPh 358
Db 1569 AACCTTTTGG---AATCTGGGCTACTGGCTGTCTATCAACAGCAGCCGCTGAACCCGT 1625

QY 358 eLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeu-Cys---- 376
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Db 1626 GTGCTATGCTCTGTGCAACAAACATTGAGAACCACTTTCAGATGCTGCTGTGCTGCA 1685
Qy 377 --ValThrLysGlnProAlaProSerGlnThrGlnSerValSerSer 391
Db 1686 GTGTGCAAAAGAGGCGCAAGCAGCAGTACGAGCAGAGACAGT 1732
RESULT 7
US-11-124-368A-14
; Sequence 14, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1974
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-368A-14
Alignment Scores:
Pred. No.: 5.28e-26 Length: 1974
Score: 405.00 Matches: 141
Percent Similarity: 41.7% Conservative: 83
Best Local Similarity: 26.3% Mismatches: 159
Query Match: 19.8% Indels: 155
DB: 14 Gaps: 19
US-10-626-126-9 (1-391) x US-11-124-368A-14 (1-1974)
Qy 2 SerGluSerAsnGlyThrAspValLeuProLeuThrAlaGln-----Val 16
Db 148 TCCTCTCCAGACGGTACCACCGATGACCCCTCTGGAGGTGCATACCGCTGCGCAAGTGGTC 207
Qy 17 ProLeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaVal 36
Db 208 TTCAATCGCTTCTTAAACGGGCATCTGCGCTTGTGTGACCATCATCGGCAACATCTCTGGA 267
Qy 37 IleLeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsn 56
Db 268 ATTGTGTCAATTAAGGTCAACAGCAGCTGAAGACGGTCAACAACACTACTTCTCTTAAGC 327
Qy 57 LeuAlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThr 76
Db 328 CTGCGCTGTGCGCATCTGATATATCGGGGTCAATTCATGAATCTGTTTACGACCTATAC 387
Qy 77 LeuPheAsn---TrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyr 95
Db 388 ATCATGTAATGATGGGCTTAGGGAATCTGGCTGTGACCTCTGGCTTGCATGACTAC 447
Qy 96 LeuLeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSer 115
Db 448 GTAGCCAGCAATGCTCTGTTATGAATCTTCTGTCATCAGCTTTGACAGATCTTTTCC 507
Qy 116 ValSerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGln 135
Db 508 ATCAGGAGCGGCTCAGTACCGAGCAACGACAA-----ACAAAGAGAGCGGTGTG 561
Qy 136 MetValAlaVal---TrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSer 154
Db 562 ATGATCGGTCTGGCTGGGTCAATCTCTCTTTGCTTTTGGGCTCTCTGCCATCTTG----- 615

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Qy 155 AspSerTrp-----LysAsnSerThrAsnThrGluGluCysGluProGly 169
Db 616 ---TTCTGGCAATACTTTGTGGAAAGAGAACTGTGCTCGGGAGAGTGTCTCATTTCAAG 672
Qy 170 PheValThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProVal 189
Db 673 TTCTCAGTGAGGCCACCATTAATTTTGGGCACGCCATCGCTGCTTTTATATGCTGTC 732
Qy 190 SerLeuValValTyrPheSerValGln----- 198
Db 733 ACCATTATGAC-TATTTTATATCTGGAGGATCTATAAGGAAACTGAAAAAGCGTACCAAGA 791
Qy 199 IleTyrTrp-----SerLeuTrpLysArgGly---SerLeuSerArgCysProSerHis 215
Db 792 GCTTGTGGCTGCTCAAGCCTCTGGACAGAGCGGACAGACAGAAAACTTTGTCCACCCAC 851
Qy 216 AlaGlyPheIleAlaThrSerSerArgGlyThrGly----- 227
Db 852 GGGCAGTTCTCGAAGCTGCAGCAGTTAGCAACTTCAACAGCAAGCATGAACCGCTCCA 911
Qy 228 -----HisSerArgArgThrGlyLeuAlaCys 236
Db 912 CAGGAGGAAGTATGGCGCTGCCACTTCTGCTTCAACAACCAAGAGCTGGAACCCAGCTC 971
Qy 237 ArgThrSer----- 239
Db 972 CGAGCAGATGGACCAAGACACAGCAGCAGTGTGGAACAACAATGATGCTGTGC 1031
Qy 240 LeuProGly-----LeuLysGluProAlaAla 248
Db 1032 CTCCTGGAGAACTCCGCTCTCCGACGAGGAGGACATTTGGTCCGAGAGAGAGCAT 1091
Qy 249 SerLeuHisSerGluSerProArgGlyLys-SerSerLeuLeuValSerLeuArgThrHi 268
Db 1092 CTACTCCATCGTCTCAAGCTTCGGGTTCACAGCACCCTCTCACTCCCAAGTTACC 1151
Qy 268 sMetSerGlySerIle-----Il 274
Db 1152 CTCATCGGACAACTTCAGAGTGCCTGAGGAGGAGCTGGGATGGTGGACTTGGAGAGAA 1211
Qy 274 eAlaPheLysVal-----GlySerPheCysArgSer-- 284
Db 1212 AGCCGACAACTGCAGGCCCAGAGAGCTGTGGAGCGATGGAGGAGCATTTTCCAAAAGCTT 1271
Qy 285 -----GluSerProVal----- 288
Db 1272 CTCCAAGCTTCCCATCCAGCTAGAGTCAGCGTGGACACAGCTTAAGACTTCTGACGTCAA 1331
Qy 288 ----- 288
Db 1332 CTCCTCAGTGGTAAAGACAGCAGGCCACTCTACCTCTCTCTTCAAGGAAGCCACTCTGGC 1391
Qy 289 -----LeuHisGlnArgGluHisValGluLeuLe 298
Db 1392 CAAGAGTTTGTCTCTGAAGACCAAGAGTCAAGTCACTTAAGCGGAAAGAGTCCCTGGT 1451
Qy 298 uArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTr 318
Db 1452 CAAGGAGAGAAGCGGCCAGACCTCAGTGCATCTTGTGCTTTCATCATCACTTG 1511
Qy 318 pAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLy 338
Db 1512 GACCCCATACATCATCATGTTCTGTGTG---AACACCTTTTGTGACAGCTGCATACCCAA 1568
Qy 338 sSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPh 358
Db 1569 AACTTTTGTG---AATCTGGGTACTGGCTGTGCTACATCAACAGACCGTGAACCCGT 1625
Qy 358 eLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeu-Cys--- 376
Db 1626 GTCTATGCTCTGTGCAACAAACATTCAGAACCACTTTCAGATGCTGTGCTGTGCCA 1685

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QY 377 --ValThrLysGlnProAlaProSerGlnThrGlnSerValSerSer 391
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Db 1686 GTGTGACAAAAAAGAGGCGCAGCAGCAGTACCAGCAGACAGT 1732

RESULT 8

US-11-136-527-2435
; Sequence 2435, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2435
; LENGTH: 2733
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2435

Alignment Scores:
Pred. No.: 1,82e-25 Length: 2733
Score: 401.00 Matches: 135
Percent Similarity: 42.0% Conservative: 84
Best Local Similarity: 25.9% Mismatches: 137
Query Match: 19.6% Indels: 166
DB: 14 Gaps: 23

US-10-626-126-9 (1-391) x US-11-136-527-2435 (1-2733)

QY 2 SerGluSerAsnGlyThrAspValLeuProLeuThrAlaGln----- 15
|||
Db 998 AGCAGCTCAACGGCACC-----CCGTAATACCCAGCGCTTGGAAAGCCATGGA 1048

QY 16 -----ValProLeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIle 31
::: |||
Db 1049 CTGTGGAGTCAATTACTATTGCACTTGTGACCTGGTGGTGCAGCTGATGACCATTTGC 1108

QY 32 GlyAsnAlaValIleLeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsn 51
|||
Db 1109 GGCATATGCTGTGTGATGATCTCTTCAAGTCAACAGTGCAGCTCAGACAGTATCAAC 1168

QY 52 TyrPhePheLeuAsnLeuAlaIleSerAspPheValGlyValIleSerIleProLeu 71
|||
Db 1169 TACTACCTGCTCAGCTTGGCTGTGCAGACCTCATCATTTGGCATCTTCTCCATGAACCTC 1228

QY 72 TyrIleProHisThrLeuPhe-----AsnTrpAsnProGlySerGlyIleCysMetPheTrp 90
::: |||
Db 1229 TACACAGCTACATCTCTCTGGGACGCTGGGTTCTCGGGAGTCTGGCTTGTGACCTTTGG 1288

QY 91 LeuIleThrAspTyrLeuLeuLeuCysThrAlaSerValTyrSerIleValLeuIleSerTyr 110
|||
Db 1289 CTGGCTCGACATGATGAGCCAGCAATGCTCTGTATGAACCTTCTGGGATAGTTT 1348

QY 111 AspArgTyrGlnSerValSerAsnAlaValArgTyrArgAlaGlnHisThr----- 127
|||
Db 1349 GATCGTTACTTTTCCATCACAGACCACTACGCTACCGGCGCAAGCGTACCCCAAGAGG 1408

QY 128 ---GlyIleLeuLysIleValAlaGlnMetValAlaValTrpIleLeuAlaPheLeuVal 146
|||
Db 1409 GCTGGCATCATGATGGCTTTAGCA-----TGGGCTGGTCTCTCTTCATCCTC 1453

QY 147 AsnGlyProMetIleLeuAlaSerAspSerTrp-----LysAsnSerThr 161
|||
Db 1454 TGGGCGCCAGCCATCTCTGCG-----TGGCAGTACTTGGTGGGAAGCGGACAGTA 1504

QY 162 AsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThrAla 181
::: |||

RESULT 9
US-11-136-527-2030
; Sequence 2030, Application US/11136527

Db 1505 CCACCTGATGAGTGCCAGATCCAGTTCTCTCTGAACCCACCATCACTTTTGGGAGTGCC 1564
QY 182 PheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyrTrp 201
|||
Db 1565 ATTGCTGCCTTTACATCCCTGTCCTCCGTCATGACCATCTACTTCTGCGGATCTACCGG 1624
QY 202 SerLeuTrpLysArg----- 206
|||
Db 1625 GAGACAGAGAGGCAACCAAGGACCTGGCTGACCTCCAAGTTCTGATTCTGTGGCAGAA 1684
QY 207 -----GlySerLeuSerArgCysPro--- 213
|||
Db 1685 GCCAAGAGAGAGAGGAGCCAGCTCAAGAGACCTGCTCAGATCTTTTCTAGTCCCTTAGA 1744
QY 214 -----SerHisAlaGlyPheIleAlaThrSerSerArgGly 225
|||
Db 1745 CCAGGCTGGCCAGAGAGAAAGAAATCAGCGCTCTCTGG---TCATCTCTCCCTAGAACG 1801
QY 226 ThrGlyHisSerArgArgThrGlyLeuAla----- 235
|||
Db 1802 ACCTCAACACAGAGAAAGACACCCAGGCGCACTGACCTTAAGTCTGCTGGGAAAGGCT 1861
QY 236 -----CysArgThrSerLeuProGlyLeuLysGluProAla----- 247
|||
Db 1862 GAGCAGGTTACTACCTGT---AGCAGCTACCCCTCTTTCAGAGGATGAAGCAAGCCACC 1918
QY 248 -----AlaSerLeuHisSerGluSerProArgGlyLys 258
|||
Db 1919 ACTGACCTGTCTTTTCAAAATGGTCTACAAGAGTGGCCAGGAAAGCCCG---GGGAG 1975
QY 259 SerSer-----LeuLeuValSerLeuArgThrHis----- 268
|||
Db 1976 GAATCAATACCAAGAGAGACCAAGAAACAGTTGTGAACACCCGAGTGAACACAGTGAC 2035
QY 269 -----MetSerGlySer 272
|||
Db 2036 TATGACACTCCCAATATCTTTCTGTCTCCAGCTGTCTGTCTCACAGACTCAAGAGTCAAG 2095
QY 273 IleIleAlaPheLys-----ValGlySer 280
|||
Db 2096 TGTGTTCCTATTAAGTTCCGATTTGGTGGTAAAGCCGATGGGACCCAGGAGACTAACAAT 2155
QY 281 PheCysArg-----SerGluSerPro--- 287
|||
Db 2156 GGCTGTGAAAGGTGAAATCATGCCCTGTCTCCAGTGTCCAAAGACCTTCAACA 2215
QY 288 -----ValLeuHisGln-----ArgGluHisValGluLeuLeu 298
|||
Db 2216 AAAGTCCCGATCCCAACCTCAGTCTCAATGATCAACAAAGAGAGAAATGGTTCTGGTC 2275
QY 299 ArgGlyArgGlyLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrp 318
|||
Db 2276 AAAGAGGAGAGCGGCTCAGACCTTGAGTGGCAATCTCTGCGCTTCATCATCATGG 2335
QY 319 AlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLys 338
|||
Db 2336 ACCCTTATACATCATGTGCTGGT---TCCACCTTCTGTGACAAGTGTGTCCCGCTC 2392
QY 339 SerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPhe 358
|||
Db 2393 ACCCTGTGGCAC---TTGGGTTACTGGCTGTGTATGTCAACAGCACCATCAACCCCATC 2449
QY 359 LeuTyrProLeuCysHisArgArgPheGlnLysAlaPhe----- 371
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Db 2450 TGTATGCTCTTGCAACAGAACTTTCAGGAAACCTTTTAAGCTGCTTCTCTGCGCGG 2509
QY 372 TrpLys 373
|||
Db 2510 TGGAAA 2515

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; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2030
; LENGTH: 4095
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2030

Alignment Scores:
Pred. No.: 3.36e-25 Length: 4095
Score: 400.50 Matches: 135
Percent Similarity: 40.0% Conservative: 79
Best Local Similarity: 25.2% Mismatches: 167
Query Match: 19.6% Indels: 155
DB: 14 Gaps: 18

US-10-626-126-9 (1-391) x US-11-136-527-2030 (1-4095)

QY 4 SerAsnGlyThrAspValLeuProLeuThrAlaGln-----ValProLeu 18
Db 698 TCAACGACACCTCCAGCGACCTCTCGGGGGTCCACACCATCTGGCAGTSGTCTTCATT 757
QY 19 AlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValAlaIleLeu 38
Db 758 GCCTTCTTAACYGGCTTCCTGGCATTTGGTGACCATCATTTGGCAACATCTTGTTCATTGTG 817
QY 39 AlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAla 58
Db 818 GCCTTCAAGGTCAACCAACAGCTGAAGACAGTCAACACACTACTTCTCTTAAAGCCTGGCC 877
QY 59 IleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPhe 78
Db 878 TGTGCAGACCTGATCATCGGGGTCATTTCTCAACCTGTCTACCTACCTACATCATATG 937
QY 79 Asn---TrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeu 97
Db 938 AACCGTGGGCACCTGGGGNACTTAGCCTCGACCTCTGGCTCTCCATTCATATGTGGCC 997
QY 98 CysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSer 117
Db 998 AGCAATGCTCTGTGCATGAATCTGCTGTGCATCAGCTTTGACAGGTACTTTTCCATCACT 1057
QY 118 AsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetVal 137
Db 1058 AGGCCACTACCTACCGAGCGCAAAAGAACCA-----ACAAACGASSTGGTGTGATGATT 1111
QY 138 AlaVal---TrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 1112 GGTCTGGCTGGGTGCATCTCTTGTCTATGCTATGGCTCTGCCATCTTG-----TTC 1162
QY 157 Trp-----LysAsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 1163 TGGCAATACTTGTAGGGAAGAGAACTGTGCCCCAGGAGAAATGTTTCATTTCATGTTCTG 1222
QY 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
Db 1223 AGTGAGCCCACTACCTTGGCAGCGCATCGCTGCCTTTTACATGCTGTGCACCATC 1282
QY 192 ValValTyrPheSerValGln-----IleTyr 200
Db 1283 ATGAC-TATTTTATCTGGAGGATCTATAGAACTGAGAACTGAGAGCGTACCAAGAGCTGGC 1341
QY 201 Trp-----SerLeuTrpLysArg---GlySerLeuSerArgCysProSerHisAlaGly 217
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1342 TGGCCTACAGCCTCTGGGACAGACGGGAGGAGAAACTTTGTTCACCCCAAGCAG 1401
218 Phe-----IleAlaThrSerSerArgGlyThr----- 226
1402 TTCTCGAAGCTGTAGCAGCTATGAACCTGCAACAGCAAGGAGGVTGAAACGATCATCCAGGAG 1461
227 -----GlyHisSerArgArgThrGlyLeuAlaCysArgThr 238
1462 GAAGTACGGTCTGCTGTCACCTTCTGGTTCACCAAGAGCTGGAAGCCCGAGCCGAGCA 1521
239 Ser-----LeuPro 241
1522 GATGGACCAAGACCACAGCAGCAGCAGCTTGGAAACAAACAGATGCTGCTGCTCCCT 1581
242 Gly-----LeuLysGluProAlaIaSerLeu 250
1582 GGAATAACTCTGCTTCTCCGATGAAGAGGACATTTGGCTCAGAGACCAAGGAGCCATCTATTTC 1641
251 HisSerGluSerProArg-GlyLysSerSerLeuValSerLeuArgThrHisMetSe 270
1642 CATTGTCTCAAGCTTTCCAGGCCATAGCTCCATCTCACTCTACCAAGCTACCTCCTC 1701
270 rGlySerIle----- 273
1702 AGATAAAGTGCAGGTGCTCCAAAGGACCTGGGGACCTGTGGATGTGGAGAGAAATGCTCA 1761
273 ----- 273
1762 CAAGCTTCAGGCCCCAGAGAGCATGGTGATGTGTGACAACTGTGACAGAGGATTTACCAA 1821
273 ----- 273
1822 GCTTCCCATCCAGTTAGAGTCTGCTGTGGACACAGGCAAGACCTCTGACACCAACTCCTC 1881
274 -----IleAlaPheLysValGlySer----- 280
1882 GGCAGACAGACCAACCGGTACTCTACTCTGTCTTCAAGGAGGCCACCGTGGCTAAGAG 1941
281 -PheCysArgSerGluSerProValLeuHisArgGluHisValGluLeuLeuArgG1 300
1942 GTTTGCTCTCAAGACCAGAGTCAGATCACCAGCGAAGAGGATGTGCGTCTATCAAGGA 2001
300 yArgLysLeuAlaArgSerLeuAlaValLeuSerAlaPheAlaIleCysTrpAlaPr 320
2002 GAAGAAGGCGGCCAGACGCTCAGTGCCATCTTGTAGCTTCTCATCATCGTGGACCC 2061
320 oTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerI1 340
2062 CTACAACATCATGGTCTCTGGTG---AACACCTTCYGTGACAGCTGCATATCCAAACCTA 2118
340 eTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTy 360
2119 TTGG---AATCTGGGTACTGGCTGTGCTATATCAACAGCACCCTGAACCTGTGTGCTA 2175
360 rProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeu-----CysVa 377
2176 TGGCCTGTGCACAAACAAATTCAGAACCACTTCAAGAVGCTCTCTTGTGCCAGTGTGA 2235
377 lThrLysGlnProAlaProSerGlnThrGlnSerValSerSer 391
2236 CAAAGGGAAGAGGCGCAACAGCAGTACCAAGCAGAGACAGCTCG 2278

RESULT 10
US-11-127-877-5
; Sequence 5, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merckhiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. P.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
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; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1495
; LENGTH: 3578
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_012527
US-11-036-196-1495

Alignment Scores:
Pred. No.: 3,48e-25 Length: 3578
Score: 399.50 Matches: 136
Percent Similarity: 40.1% Conservative: 80
Best Local Similarity: 25.3% Mismatches: 162
Query Match: 19.5% Indels: 161
DB: 11 Gaps: 18

US-10-626-126-9 (1-391) x US-11-036-196-1495 (1-3578)

QY 4 SerAsnGlyThrAspValLeuProLeuThrAlaGln-----ValProLeu 18
DB 191 TCACACACACCTCCAGCGACCTCTCGGGGTGACACCATCTGGCAAGTGGTTCATT 250
QY 19 AlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeu 38
DB 251 GCCTTCTAACTGGCTTCCTGGCATGTTGTCACCATCATTTGGCAACATCTTGTTCATTGTG 310
QY 39 AlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAla 58
DB 311 GCCTTCAAGGTCACAAACACAGCTGAAGACAGATCAACAACTACTTCTTTAAGCCTGGCC 370
QY 59 IleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPhe 78
DB 371 TGTGCAGACCTGATCATCGGGTCAATTCATGAACTGTCACCTGTCATCATCATCATTTATG 430
QY 79 Asn---TrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeu 97
DB 431 AACCGTTGGGCACCTGGGGAACCTTAGCTGGACCTCTGGCTCTCCATTGACTATGTGGCC 490
QY 98 CysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSer 117
DB 491 AGCAATGCCCTGTGTCATGAATCTGCTGTCATCAGCTTTCACAGGTACTTTTCATCACT 550
QY 118 AsnAlaValArgTyrArgAlaGlnHisThr-----GlyIleLeuIleVal 133
DB 551 AGGCCACTACCTACCGAGCCAAAGAACACAAACAGACGTGGTGTGATGATTGGTCTG 610
QY 134 AlaGlnMetValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAla 153
DB 611 GCT-----TGGGTCACTCTCTTGTCTATGGGCTCTGTCACCTTG--- 652
QY 154 SerAspSerTrp-----LysAsnSerThrAsnThrGluGluCysGluPro 168

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DB 653 -----TTCTGGCAATACTTTGTAGGAAGAAGAACTGTGCCCCCAGGAGATGTTTCATT 706
QY 169 GlyPheValThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuPro 188
DB 707 CAGTTTCTGAGTGAGCCACCATCATCCTTCGGCAGCGCATCGCTGCTTTTACATGCT 766
QY 189 ValSerLeuValValTyrPheSerValGln----- 198
DB 767 GTCCACCATCATGAC-TATTTTATCTGGAGGATCTATAAGGAAACTGAGAAGCCTACCAA 825
QY 199 ---IleTyrTrp-----SerLeuTrpLysArg---GlySerLeuSerArgCysProSer 214
DB 826 AGAGCTGGCTGGCTACAGSCCTCTGGACAGAAGCGGAGGCAGAAAACTTTGTCACCC 885
QY 215 HisAlaGlyPhe-----IleAlaThrSerSerArgGlyThr--- 226
DB 886 CACAGGCAGTTCTCGAAGCTGTAGCAGCTATGAACATGCAACAGCAGCGGTGAACGATC 945
QY 227 -----GlyHisSerArgArgThrGlyLeuAla 235
DB 946 ATCCAGGAGGAAGTACGTCGCTGTCTACTTCTGTTCCACCACCAAGAGCTGGAAGCCGAG 1005
QY 236 CysArgThrSer----- 239
DB 1006 TGGCAGCAGATGAGCCACCAAGCAGCAGCAGCAGCAGTGGNACAAACACGATGCTGC 1065
QY 240 ---LeuProGly-----LeuLysGluProAla 247
DB 1066 TGCTCTCCCTGGAACACTCTGCTTCTCCGATGAAGAGGACATGCTGCTCAGAGACCGAGGC 1125
QY 248 AlaSerLeuHisSerGluSerProArg-GlyLysSerSerLeuValSerLeuArgTh 267
DB 1126 CATCTATTCCATTTGCTCCTCAAGCTTCCAGGCCATAGCTCCATCTCAACTCTACCAAGCT 1185
QY 267 rHisMetSerGlySerIle----- 273
DB 1186 ACCGTCTCTCAGATAACCTGCAGGTGTCCAAGAGGACCTGGGACTGTGGATGTGGAGAG 1245
QY 273 ----- 273
DB 1246 AATGCTCACAAGCTTCAGGCCCCAGAGAGCATGGGTGATGGTGACAACCTGTGAGAAGGA 1305
QY 273 ----- 273
DB 1306 TTTTACCAGCTTCCCATCCAGTTAGAGTCTGCGTGTGACACACAGCGAAGACCTCTGACAC 1365
QY 274 -----IleAlaPheLysValGlySer-- 280
DB 1366 CAACTCTCGGCAGACAAAGACACCGGCTACTCTACCTCTGTCTCTTCAAGGAGGCCACGCT 1425
QY 281 -----PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLe 297
DB 1426 GGCTAAGAGGTTTGTCTCTCAAGACCAAGAGTCAGATCACCAAGCGGAAGAGGATGTCGCT 1485
QY 297 uLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCy 317
DB 1486 CATCAAGGAGAGAAGCGCCGCGCAGCGCTCAGTGCATCTTGTAGCTTTCATCATCAC 1545
QY 317 sTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgPr 337
DB 1546 GTGGACCCCTTACAACATCATGTGCTGGTG---AACCTCTCTGTGACAGCTGCATACC 1602
QY 337 oLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnPr 357
DB 1603 CAAAACCTATTGG---AATCTGGGTACTGCTGCTGTGTATATCAACAGCAGCCGGAACCC 1659
QY 357 oPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeu----- 375
DB 1660 TGTGTGCTATGCTGTGCAACAAACATTCAGAACCCACCTTCAAGACGCTCTCTTGTG 1719
QY 376 ---CysValThrLysGlnProAlaProSerGlnThrGlnSerValSerSer 391

```



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;
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 2806
; LENGTH: 4061
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-2806

Alignment Scores:
Pred. No.: 7,12e-23 Length: 4061
Score: 374.50 Matches: 104
Percent Similarity: 46.1% Conservative: 62
Best Local Similarity: 28.9% Mismatches: 141
Query Match: 18.3% Indels: 53
DB: 14 Gaps: 12

US-10-626-126-9 (1-391) x US-11-136-527-2806 (1-4061)
QY 24 LeuLeuAlaPheAlaIleThr-----IleGlyAsnAlaValValIleLeuAlaPheVal 41
Db 1885 CTGGCGGCTTCTATCTCTACCGCTGGCGGGACACTGCTGTCTATCTTTCGTGGGCC 1944
QY 42 AlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSerAsp 61
Db 1945 TGCAACCGCCACCTACAGACGGTCAACCACTATTCTCATCGTAACCTGGCGGTGGCTGAC 2004
QY 62 PhePheValGlyValIleSerIleProLeuTyrIlePro---HisThrLeuPheAsnTyr 80
Db 2005 CTGCTTTTGAGTCAGCTGTGTTGCCCTTCTTCAGCCACTATGGAGGTTCTTAGGCTTCTGG 2064
QY 81 AsnProGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 2065 GCCTTCGGCGGAACCTCTTCGACGCTGGCGCGGTGGAGCTGTGTGTGCTGCACTGCC 2124
QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 2125 TCCATCTTAGCTCTGCACCACTCTCTGTGACCGGTAGCTGGGTGTGGCCACTGGCTC 2184
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
Db 2185 AGTACCCAGCCATTATGACAGAG---CGCAAGGCGCTGCCATTCTGGCTCTGCTTTGG 2241
QY 141 IleLeuAlaPheLeuValAsn---GlyProMetIleLeuAlaSerAspSerTyrLysAsn 159
Db 2242 GCGGTGGCTGTGTGTATCTGTGGACCGCTACTA-----GGTTGGAGGAG 2289
QY 160 SerThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTyrIleLeuAlaIle 179
Db 2290 CCAGTCCCCCGAGCTTCTTCGGGCATCACCAGAGGAGGTGGCTATGCAATCTTC 2349
QY 180 ThrAlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIle 199
Db 2350 TCTTCGCTGTCTCTCTTCTACCTACCATGGCAGTATCGTGTGCTCATCTCCCGCTG 2409
QY 200 TyrTyrSerLeuTyrLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIle 219
Db 2410 TAC----- 2412
QY 220 AlaThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSer 239
Db 2413 ---GTGGTCGACGCGCACTACGCGCAGCTCTCGAGCAGGATCAAG----- 2457
QY 240 LeuProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSer 259
Db 2458 -----AGGAGGCC-----GGCAAGGCC 2475

RESULT 15
US-11-136-527-2806
; Sequence 2806, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
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;
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 2806
; LENGTH: 4061
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-2806

Alignment Scores:
Pred. No.: 7,12e-23 Length: 4061
Score: 374.50 Matches: 104
Percent Similarity: 46.1% Conservative: 62
Best Local Similarity: 28.9% Mismatches: 141
Query Match: 18.3% Indels: 53
DB: 14 Gaps: 12

US-10-626-126-9 (1-391) x US-11-136-527-2806 (1-4061)
QY 24 LeuLeuAlaPheAlaIleThr-----IleGlyAsnAlaValValIleLeuAlaPheVal 41
Db 1885 CTGGCGGCTTCTATCTCTACCGCTGGCGGGACACTGCTGTCTATCTTTCGTGGGCC 1944
QY 42 AlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSerAsp 61
Db 1945 TGCAACCGCCACCTACAGACGGTCAACCACTATTCTCATCGTAACCTGGCGGTGGCTGAC 2004
QY 62 PhePheValGlyValIleSerIleProLeuTyrIlePro---HisThrLeuPheAsnTyr 80
Db 2005 CTGCTTTTGAGTCAGCTGTGTTGCCCTTCTTCAGCCACTATGGAGGTTCTTAGGCTTCTGG 2064
QY 81 AsnProGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 2065 GCCTTCGGCGGAACCTCTTCGACGCTGGCGCGGTGGAGCTGTGTGTGCTGCACTGCC 2124
QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 2125 TCCATCTTAGCTCTGCACCACTCTCTGTGACCGGTAGCTGGGTGTGGCCACTGGCTC 2184
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
Db 2185 AGTACCCAGCCATTATGACAGAG---CGCAAGGCGCTGCCATTCTGGCTCTGCTTTGG 2241
QY 141 IleLeuAlaPheLeuValAsn---GlyProMetIleLeuAlaSerAspSerTyrLysAsn 159
Db 2242 GCGGTGGCTGTGTGTATCTGTGGACCGCTACTA-----GGTTGGAGGAG 2289
QY 160 SerThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTyrIleLeuAlaIle 179
Db 2290 CCAGTCCCCCGAGCTTCTTCGGGCATCACCAGAGGAGGTGGCTATGCAATCTTC 2349
QY 180 ThrAlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIle 199
Db 2350 TCTTCGCTGTCTCTCTTCTACCTACCATGGCAGTATCGTGTGCTCATCTCCCGCTG 2409
QY 200 TyrTyrSerLeuTyrLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIle 219
Db 2410 TAC----- 2412
QY 220 AlaThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSer 239
Db 2413 ---GTGGTCGACGCGCACTACGCGCAGCTCTCGAGCAGGATCAAG----- 2457
QY 240 LeuProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSer 259
Db 2458 -----AGGAGGCC-----GGCAAGGCC 2475
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Qy 260 SerLeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLys---Val 278
Db |||:::|| ||||| ||| |||:::|| |||:::||
2476 TCCGAGGTGGTT---CTGAGATCCACTGTCCGCGCCGACGCGCCCAAGGATAT 2532

Qy 279 GlySerPheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeu 298
Db |||:::|| |||:::|| |||:::|| |||:::|| |||:::|| |||:::|| |||:::||
2533 CCCGGACACAGAGTAGCAGGGCCACACTTGGCGAGCTCGCTTCCGTGAGGCTGCTC 2592

Qy 299 -----ArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAla 315
Db |||:::|| |||:::|| |||:::|| |||:::|| |||:::|| |||:::|| |||:::||
2593 AAGTTTTCGCCGAGAAAAGGCTGCCAAGACGTTGGCCATCGTGGGTGCTTCGTC 2652

Qy 316 IleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgGlyGlu 335
Db |||:::|| |||:::|| |||:::|| |||:::|| |||:::|| |||:::|| |||:::||
2653 CTGTGCTGTTCCCTTC---TTCCTTCGCTCGCTCTGGGCTCTCTGTTCCTCCGAGCTG 2709

Qy 336 ArgProLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIle 355
Db |||:::|| |||:::|| |||:::|| |||:::|| |||:::|| |||:::|| |||:::||
2710 AACCGTCAGAGGGTGTTCTCAAGGTCACTCTCTGGCTGGGCTACTTCAATAGTGTGTG 2769

Qy 356 AsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeu 375
Db |||:::|| |||:::|| |||:::|| |||:::|| |||:::|| |||:::|| |||:::||
2770 AACCGCTCATCTACCCCTGCTCCAGTCGCGAGTCAAGCGCGCTTCTCCTCCGCTCCTG 2829
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Job time : 5410 secs

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